

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:10:17 ; Search time 117 Seconds
(without alignments)
928.510 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540
Sequence: 1 VYLSECKTGNGKNYRGTMK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	4	US-10-131-241-61 Sequence 61, Appl
2	1535	99.7	303	3	US-10-810-262-11 Sequence 11, Appl
3	1535	99.7	339	3	US-09-788-142-3 Sequence 3, Appl
4	1535	99.7	339	3	US-09-761-120-3 Sequence 3, Appl
5	1535	99.7	339	3	US-09-335-325-3 Sequence 3, Appl
6	1535	99.7	339	4	US-10-131-241-3 Sequence 3, Appl
7	1535	99.7	339	4	US-10-127-066-3 Sequence 3, Appl
8	1535	99.7	339	4	US-10-402-364-3 Sequence 3, Appl
9	1535	99.7	339	4	US-10-401-108-3 Sequence 3, Appl
10	1535	99.7	363	4	US-10-292-418-11 Sequence 11, Appl
11	1535	99.7	378	3	US-09-873-676-1 Sequence 1, Appl
12	1535	99.7	378	3	US-09-335-325-42 Sequence 42, Appl
13	1535	99.7	378	4	US-10-131-241-42 Sequence 42, Appl
14	1535	99.7	378	4	US-10-127-066-42 Sequence 42, Appl
15	1535	99.7	391	4	US-10-304-287-7 Sequence 7, Appl
16	1535	99.7	391	4	US-10-415-012-1 Sequence 1, Appl
17	1535	99.7	391	4	US-10-735-577-7 Sequence 7, Appl
18	1535	99.7	394	4	US-10-304-287-8 Sequence 8, Appl
19	1535	99.7	394	4	US-10-415-012-2 Sequence 2, Appl
20	1535	99.7	394	4	US-10-735-577-8 Sequence 8, Appl
21	1535	99.7	484	4	US-10-135-872B-7 Sequence 7, Appl
22	1535	99.7	567	4	US-10-741-601-413 Sequence 413, App
23	1535	99.7	569	3	US-09-946-893-5 Sequence 5, Appl
24	1535	99.7	571	3	US-09-946-893-8 Sequence 8, Appl
25	1535	99.7	576	3	US-09-946-893-6 Sequence 6, Appl
26	1535	99.7	579	4	US-10-449-609-7 Sequence 7, Appl
27	1535	99.7	714	4	US-10-415-012-8 Sequence 8, Appl

28	1535	99.7	714	5	US-10-503-910-18 Sequence 18, Appl
29	1535	99.7	791	3	US-09-967-386-1 Sequence 1, Appl
30	1535	99.7	791	4	US-10-304-287-1 Sequence 1, Appl
31	1535	99.7	791	4	US-10-360-101-257 Sequence 257, App
32	1535	99.7	791	4	US-10-778-423-1 Sequence 1, Appl
33	1535	99.7	791	4	US-10-753-646-1 Sequence 1, Appl
34	1535	99.7	791	4	US-10-735-577-1 Sequence 1, Appl
35	1535	99.7	791	5	US-10-729-475-10 Sequence 10, Appl
36	1535	99.7	791	5	US-10-503-910-17 Sequence 17, Appl
37	1535	99.7	799	5	US-10-503-910-8 Sequence 8, Appl
38	1535	99.7	803	5	US-10-503-910-10 Sequence 10, Appl
39	1535	99.7	810	3	US-09-946-893-2 Sequence 2, Appl
40	1535	99.7	810	4	US-10-193-656-2 Sequence 2, Appl
41	1535	99.7	810	4	US-10-237-144-1 Sequence 1, Appl
42	1535	99.7	810	4	US-10-135-872B-4 Sequence 4, Appl
43	1535	99.7	810	4	US-10-450-976-2 Sequence 2, Appl
44	1535	99.7	810	4	US-10-415-012-4 Sequence 4, Appl
45	1535	99.7	810	4	US-10-741-601-409 Sequence 409, App

ALIGNMENTS

```
RESULT 1
US-10-131-241-61
; Sequence 61, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Fortier, John W.
; APPLICANT: Fortier, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-61
Query Match 100.0%; Score 1540; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.1e-120; Mismatches 0; Indels 0; Gaps 0;
Matches 260; Conservative 0;

1 VYLSECKTGNGKNYRGTMKSTKNGITCQKMSSTSPHRRPSPATPSSEGLSENYCRNPON 60
1 VLSCKTGNGKNYRGTMKSTKNGITCQKMSSTSPHRRPSPATPSSEGLSENYCRNPON 60
61 DPGWCVTTTDEPKRYDCDILECEBECMGHSGENYDGIKSTMSGLBQAWDSOPHMH 120
61 DPGWCVTTTDEPKRYDCDILECEBECMGHSGENYDGIKSTMSGLBQAWDSOPHMH 120
121 GTTPKFPKNLKKKNCNPNRELAPMCTTDPNKRMBLCDIPRCTTPSSGPTCYCLK 180
121 GTTPKFPKNLKKKNCNPNRELAPMCTTDPNKRMBLCDIPRCTTPSSGPTCYCLK 180
121 GTTPKFPKNLKKKNCNPNRELAPMCTTDPNKRMBLCDIPRCTTPSSGPTCYCLK 180
181 GTGENYRGNAVAVTYSGHTCOHWSAQTPTHTERTPENFCKNLDENYCRNPDGKRAPWCHT 240
181 GTGENYRGNAVAVTYSGHTCOHWSAQTPTHTERTPENFCKNLDENYCRNPDGKRAPWCHT 240
241 TNSQVRWEYCKIPSCDSSPV 260
241 TNSQVRWEYCKIPSCDSSPV 260
241 TNSQVRWEYCKIPSCDSSPV 260
```

```
RESULT 2
US-10-810-262-11
; Sequence 11, Application US/10810262
; Publication No. US20040234505A1
; GENERAL INFORMATION:
; APPLICANT: KINGSMAN, SUSAN MARY
; APPLICANT: NAVIOL, STUART
; APPLICANT: BINFLEY, KATIE
; TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
; FILE REFERENCE: 674523-2029.1
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/810,262
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/GB99/03181
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/GB98/02885
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: GB 9901906.9
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: GB 9903538.8
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 11
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-810-262-11

Query Match          99.7%; Score 1535; DB 5; Length 303;
Best Local Similarity 99.6%; Pred. No. 6,5e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGYRGTMSTKNGITCQKMSSTSPHRPFSPATHPBSGLSEENYCRNPDN 60
DB 33 VYLSECKTGNKNGYRGTMSTKNGITCQKMSSTSPHRPFSPATHPBSGLSEENYCRNPDN 92

QY 61 DPGGWCCTTDPBKKYDYCDILCEBECMHSGENYDGIKSTMSGLBEOANDSOPHMH 120
DB 93 DPGGWCCTTDPBKKYDYCDILCEBECMHSGENYDGIKSTMSGLBEOANDSOPHMH 152

QY 121 GYIPSKFPNKNLKKNYCRNPDELAPWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCLK 180
DB 153 GYIPSKFPNKNLKKNYCRNPDELAPWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCLK 212

QY 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 213 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 272

QY 241 TNSOVMEYCKIIPSCDSSPV 260
DB 273 TNSOVMEYCKIIPSCDSSPV 292

RESULT 3
US-09-788-142-3
; Sequence 3, Application US/09788142
; Patent No. US20010029246A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-788-142-3

Query Match          99.7%; Score 1535; DB 3; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGYRGTMSTKNGITCQKMSSTSPHRPFSPATHPBSGLSEENYCRNPDN 60
DB 1 VYLSECKTGNKNGYRGTMSTKNGITCQKMSSTSPHRPFSPATHPBSGLSEENYCRNPDN 60

QY 61 DPGGWCCTTDPBKKYDYCDILCEBECMHSGENYDGIKSTMSGLBEOANDSOPHMH 120
DB 61 DPGGWCCTTDPBKKYDYCDILCEBECMHSGENYDGIKSTMSGLBEOANDSOPHMH 120

QY 121 GYIPSKFPNKNLKKNYCRNPDELAPWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCLK 180
DB 121 GYIPSKFPNKNLKKNYCRNPDELAPWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCLK 180

QY 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240

QY 241 TNSOVMEYCKIIPSCDSSPV 260
DB 241 TNSOVMEYCKIIPSCDSSPV 260

RESULT 4
US-09-761-120-3
; Sequence 3, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringles 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT FILING DATE: US/09/761,120
; PRIOR APPLICATION NUMBER: 2001-01-16
; PRIOR FILING DATE: 1999-05-11
```

; PRIOR APPLICATION NUMBER: 08/866,735
 ; PRIOR FILING DATE: 1997-05-30
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-761-120-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNYRGTMKTKNGITTCQWSTSPHRRPSPATPSSGLEENYCRNPDN 60
 DB 1 VLSCKTGNGKNYRGTMKTKNGITTCQWSTSPHRRPSPATPSSGLEENYCRNPDN 60
 QY 61 DPGFWCTTDPBEKRYDCDILECEBECMHCSGENYDKISKTMGSLCQAMDSOPH 120
 DB 61 DPGFWCTTDPBEKRYDCDILECEBECMHCSGENYDKISKTMGSLCQAMDSOPH 120
 QY 121 GIYPSKFPNNKLKNYCRNPDELPCWCTTDPNKRMEICDIPRCTPPSSGPTYQCL 180
 DB 121 GIYPSKFPNNKLKNYCRNPDELPCWCTTDPNKRMEICDIPRCTPPSSGPTYQCL 180
 QY 181 GTGENYRGNVAVTYSGHTCQWMSAQTPTHRTPTNPFCCKNDENYCRNPDKRAPWCHT 240
 DB 181 GTGENYRGNVAVTYSGHTCQWMSAQTPTHRTPTNPFCCKNDENYCRNPDKRAPWCHT 240
 QY 241 TNSQVMEYCKIPSCDSSPV 260
 DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 5

US-09-335-325-3
 ; Sequence 3, Application US/09335325
 ; Patent No. US20020164717A1
 ; GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah
 O'Reilly, Michael
 Cao, Yihai

TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia

COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 339 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: Angiostatin fragment
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-335-325-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNYRGTMKTKNGITTCQWSTSPHRRPSPATPSSGLEENYCRNPDN 60
 DB 1 VLSCKTGNGKNYRGTMKTKNGITTCQWSTSPHRRPSPATPSSGLEENYCRNPDN 60
 QY 61 DPGFWCTTDPBEKRYDCDILECEBECMHCSGENYDKISKTMGSLCQAMDSOPH 120
 DB 61 DPGFWCTTDPBEKRYDCDILECEBECMHCSGENYDKISKTMGSLCQAMDSOPH 120
 QY 121 GIYPSKFPNNKLKNYCRNPDELPCWCTTDPNKRMEICDIPRCTPPSSGPTYQCL 180
 DB 121 GIYPSKFPNNKLKNYCRNPDELPCWCTTDPNKRMEICDIPRCTPPSSGPTYQCL 180
 QY 181 GTGENYRGNVAVTYSGHTCQWMSAQTPTHRTPTNPFCCKNDENYCRNPDKRAPWCHT 240
 DB 181 GTGENYRGNVAVTYSGHTCQWMSAQTPTHRTPTNPFCCKNDENYCRNPDKRAPWCHT 240
 QY 241 TNSQVMEYCKIPSCDSSPV 260
 DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 6

US-10-131-241-3
 ; Sequence 3, Application US/10131241
 ; Publication No. US20030012792A1
 ; GENERAL INFORMATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation

FILE REFERENCE: 05213-0344 43170-271565

CURRENT FILING DATE: 2002-07-22

PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens

US-10-131-241-3

Query Match 99.7%; Score 1535; DB 4; Length 339;

Best Local Similarity 99.6%; Pred. No. 7.4e-120;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VLSCKTGNGKNYRGTMKTKNGITTCQWSTSPHRRPSPATPSSGLEENYCRNPDN 60

|||||

|||||

|||||

|||||

|||||

```

Db      1  VLSBCKTGNGKNGTGMSTKNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
Qy      61  DPGWMCYTTPBPKRYDYCDILECEBECMHCSGSENYDCKISKTMSGLBEOAMDOSPHAH 120
Db      61  DPGWMCYTTPBPKRYDYCDILECEBECMHCSGSENYDCKISKTMSGLBEOAMDOSPHAH 120
Qy      121  GYIPSKFPNKNLKKNYCNRNPDRELPRMCFITTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Db      121  GYIPSKFPNKNLKKNYCNRNPDRELPRMCFITTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Qy      181  GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCNRPDGRAPMCHT 240
Db      181  GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCNRPDGRAPMCHT 240
Qy      241  TNSQVMEYCKIIPSCDSSPV 260
Db      241  TNSQVMEYCKIIPSCDSSPV 260

```

```

RESULT 7
US-10-127-066-3

```

```

; Sequence 3, Application US/10127066
; Publication No. US20030064926A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Folkman, M. Judah
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; FILE REFERENCE: 05213-0612 43170-272529
; CURRENT APPLICATION NUMBER: US/10/127,066
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-066-3

```

```

Query Match      99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 7,4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1  VLSBCKTGNGKNGTGMSTKNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
Db      1  VLSBCKTGNGKNGTGMSTKNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
Qy      61  DPGWMCYTTPBPKRYDYCDILECEBECMHCSGSENYDCKISKTMSGLBEOAMDOSPHAH 120
Db      61  DPGWMCYTTPBPKRYDYCDILECEBECMHCSGSENYDCKISKTMSGLBEOAMDOSPHAH 120
Qy      121  GYIPSKFPNKNLKKNYCNRNPDRELPRMCFITTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Db      121  GYIPSKFPNKNLKKNYCNRNPDRELPRMCFITTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Qy      181  GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCNRPDGRAPMCHT 240
Db      181  GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCNRPDGRAPMCHT 240
Qy      241  TNSQVMEYCKIIPSCDSSPV 260
Db      241  TNSQVMEYCKIIPSCDSSPV 260

```

```

RESULT 8
US-10-402-364-3
; Sequence 3, Application US/10402364
; Publication No. US20040002459A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael
; APPLICANT: Folkman, M. Judah
; TITLE OF INVENTION: Nucleic Acids Encoding Kringles 1-5 Region Fragments of Plasminogen

```

```

; FILE REFERENCE: 05213-2151 (43170-252068)
; CURRENT APPLICATION NUMBER: US/10/402,364
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/761,120A
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/309,821
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 08/866,735
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-364-3

```

```

Query Match      99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 7,4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1  VLSBCKTGNGKNGTGMSTKNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
Db      1  VLSBCKTGNGKNGTGMSTKNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
Qy      61  DPGWMCYTTPBPKRYDYCDILECEBECMHCSGSENYDCKISKTMSGLBEOAMDOSPHAH 120
Db      61  DPGWMCYTTPBPKRYDYCDILECEBECMHCSGSENYDCKISKTMSGLBEOAMDOSPHAH 120
Qy      121  GYIPSKFPNKNLKKNYCNRNPDRELPRMCFITTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Db      121  GYIPSKFPNKNLKKNYCNRNPDRELPRMCFITTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Qy      181  GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCNRPDGRAPMCHT 240
Db      181  GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCNRPDGRAPMCHT 240
Qy      241  TNSQVMEYCKIIPSCDSSPV 260
Db      241  TNSQVMEYCKIIPSCDSSPV 260

```

```

RESULT 9
US-10-401-108-3

```

```

; Sequence 3, Application US/10401108
; Publication No. US20040023877A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/401,108
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,735
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren, William L.
; REGISTRATION NUMBER: 36,714

```

REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-401-108-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGKNGYGTMSKTNGITTCQKMSSTSPHPPSPATHPSEGLSENYCNPND 60
DB 1 VYLSECKTGNKNGKNGYGTMSKTNGITTCQKMSSTSPHPPSPATHPSEGLSENYCNPND 60
QY 61 DPQGPWCYTTPDEKRYDYCDILECEBECMHCNGENYDGKISKTMSGLECOAMDOSPHAH 120
DB 61 DPQGPWCYTTPDEKRYDYCDILECEBECMHCNGENYDGKISKTMSGLECOAMDOSPHAH 120
QY 121 GYIPSKFPKKNLKKYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCLK 180
DB 121 GYIPSKFPKKNLKKYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHRTPEHPCKNDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHRTPEHPCKNDENYCRNPDGRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 10
US-10-292-418-11
Sequence 11, Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/383,315
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-418-11

Query Match 99.7%; Score 1535; DB 4; Length 363;
Best Local Similarity 99.6%; Pred. No. 8e-120;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNKNGKNGYGTMSKTNGITTCQKMSSTSPHPPSPATHPSEGLSENYCNPND 60
DB 2 VYLSECKTGNKNGKNGYGTMSKTNGITTCQKMSSTSPHPPSPATHPSEGLSENYCNPND 61
QY 61 DPQGPWCYTTPDEKRYDYCDILECEBECMHCNGENYDGKISKTMSGLECOAMDOSPHAH 120
DB 62 DPQGPWCYTTPDEKRYDYCDILECEBECMHCNGENYDGKISKTMSGLECOAMDOSPHAH 121
QY 121 GYIPSKFPKKNLKKYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCLK 180
DB 122 GYIPSKFPKKNLKKYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCLK 181
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHRTPEHPCKNDENYCRNPDGRAPWCHT 240
DB 182 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHRTPEHPCKNDENYCRNPDGRAPWCHT 241
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 11
US-09-873-676-1
Sequence 1, Application US/09873676
Patent No. US20020077289A1
GENERAL INFORMATION:
APPLICANT: Macdonald, Nicholas J.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
FILE REFERENCE: 05213-0378 (43170-259333)
CURRENT APPLICATION NUMBER: US/09/873,676
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 60/209,065
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/289,387
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-873-676-1

Query Match 99.7%; Score 1535; DB 3; Length 378;
Best Local Similarity 99.6%; Pred. No. 8.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGKNGYGTMSKTNGITTCQKMSSTSPHPPSPATHPSEGLSENYCNPND 60
DB 6 VYLSECKTGNKNGKNGYGTMSKTNGITTCQKMSSTSPHPPSPATHPSEGLSENYCNPND 65
QY 61 DPQGPWCYTTPDEKRYDYCDILECEBECMHCNGENYDGKISKTMSGLECOAMDOSPHAH 120
DB 66 DPQGPWCYTTPDEKRYDYCDILECEBECMHCNGENYDGKISKTMSGLECOAMDOSPHAH 125
QY 121 GYIPSKFPKKNLKKYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCLK 180
DB 126 GYIPSKFPKKNLKKYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCLK 185
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHRTPEHPCKNDENYCRNPDGRAPWCHT 240
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHTHRTPEHPCKNDENYCRNPDGRAPWCHT 245
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 12
US-09-335-325-42

```

Sequence 42, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkmann, M. Judah
O'Reilly, Micheal
Cao, Yihai
Slim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marten, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: KI-4BK5
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-335-325-42
Query Match 99.7%; Score 1535; DB 3; Length 378;
Best Local Similarity 99.6%; Pred. No. 8 4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Db 1 VYLSECKTGNGKNGYGTMSKTNGLTCQKMSSTSPHRRPSPATHPBSGLBENYCRNPDN 60
6 VYLSCKTGNGKNGYGTMSKTNGLTCQKMSSTSPHRRPSPATHPBSGLBENYCRNPDN 65
QY 61 DPQGWCTTTPDKRYDYCDIIECBECBCHGSGENTYDKISTKMSGLBEOAMDSDSPAHN 120
Db 66 DPQGWCTTTPDKRYDYCDIIECBECBCHGSGENTYDKISTKMSGLBEOAMDSDSPAHN 125
QY 121 GYIPKFPKKNLKKNYCRNPDBELRPWCFTTDPNKRWECDIPRCTTTPPSGPTTQCK 180
Db 126 GYIPKFPKKNLKKNYCRNPDBELRPWCFTTDPNKRWECDIPRCTTTPPSGPTTQCK 185
QY 181 GTGENYRGVAVTVSGHTCQHMSAQTPTHTERTPENFPCKNDENYCRNPDGRAPWCHT 240
Db 186 GTGENYRGVAVTVSGHTCQHMSAQTPTHTHTRTPENFPCKNDENYCRNPDGRAPWCHT 245
QY 241 TNSQVRWEYCKIPSCDSFV 260

```

```

Db      246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 13
US-10-131-241-42
; Sequence 42, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; APPLICANT: Fortler, Anne H.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
; FILE REFERENCE: 05213-0344 43170-271565
; CURRENT APPLICATION NUMBER: US/10/131,241
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/413,049
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 09/316,802
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/086,586
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-42

Query Match          99.7%; Score 1535; DB 4; Length 378;
Best Local Similarity 99.6%; Pred. No. 8,4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VYLSSECTGNGKNGKRGMTSGTKNGITGQKNSSTGSPHRRPSPATHPSEGLEBNYCRNPDN 60
DB      6 VYLSSECTGNGKNGKRGMTSGTKNGITGQKNSSTGSPHRRPSPATHPSEGLEBNYCRNPDN 65
QY      61 DPQSPWCYTTDPERKRYIYCDILBCEBECMHCSGENYNGKISKTMSSGLEQAMPSQSPHAA 120
DB      66 DPQSPWCYTTDPERKRYIYCDILBCEBECMHCSGENYNGKISKTMSSGLEQAMPSQSPHAA 125
QY      121 GYISKCPNNKLNKKNYCRNPDRELRPWCFTTDPKRWELCDIPRCTPPPSGPTYOCLK 180
DB      126 GYISKCPNNKLNKKNYCRNPDRELRPWCFTTDPKRWELCDIPRCTPPPSGPTYOCLK 185
QY      181 GTGENYGNVAVTVSGTCHOWMSAQTPHTHERTPENPPCKNLDEMYCRNPDGKAPWCHT 240
DB      186 GTGENYGNVAVTVSGTCHOWMSAQTPHTHTNRPTEPPCKNLDEMYCRNPDGKAPWCHT 245
QY      241 TNSQVRWEYCKIPSCDSSPV 260
DB      246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 14
US-10-127-066-42
; Sequence 42, Application US/10127066
; Publication No. US20030064926A1
; GENERAL INFORMATION:
; APPLICANT: O'Reilly, Michael S.
; APPLICANT: Folkman, M. Judah
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; FILE REFERENCE: 05213-0612 43170-272529
; CURRENT APPLICATION NUMBER: US/10/127,066
; CURRENT FILING DATE: 2002-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 378
; TYPE: PRT

```

ORGANISM: Homo sapiens
US-10-127-066-42

Query Match 99.7%; Score 1535; DB 4; Length 378;
Best Local Similarity 99.6%; Pred. No. 8.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNGKNGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 60
DB 6 VYLSECKTNGKNGKNGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 65
QY 61 DPGFWCYTTDPKRYDYCDILECEBECNHGSGENYDGKISKTMGSLGCQAWDSQSPHAA 120
DB 66 DPGFWCYTTDPKRYDYCDILECEBECNHGSGENYDGKISKTMGSLGCQAWDSQSPHAA 125
QY 121 GYIPSKFPKKNLKKNYCRNPDRRLRPWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
DB 126 GYIPSKFPKKNLKKNYCRNPDRRLRPWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 185
QY 181 GTGENYRGNAVATVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240
DB 186 GTGENYRGNAVATVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 245
QY 241 TNSQVRMEYCKIPSCDSSPV 260
DB 246 TNSQVRMEYCKIPSCDSSPV 265

RESULT 15

US-10-304-287-7
; Sequence 7, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, Mijung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 391
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-7

Query Match 99.7%; Score 1535; DB 4; Length 391;
Best Local Similarity 99.6%; Pred. No. 8.7e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNGKNGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 60
DB 2 VYLSECKTNGKNGKNGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 61
QY 61 DPGFWCYTTDPKRYDYCDILECEBECNHGSGENYDGKISKTMGSLGCQAWDSQSPHAA 120
DB 62 DPGFWCYTTDPKRYDYCDILECEBECNHGSGENYDGKISKTMGSLGCQAWDSQSPHAA 121
QY 121 GYIPSKFPKKNLKKNYCRNPDRRLRPWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
DB 122 GYIPSKFPKKNLKKNYCRNPDRRLRPWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 181
QY 181 GTGENYRGNAVATVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240
DB 182 GTGENYRGNAVATVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 241
QY 241 TNSQVRMEYCKIPSCDSSPV 260
DB 242 TNSQVRMEYCKIPSCDSSPV 261

Search completed: January 25, 2006, 17:21:52
Job time : 118 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:04:06 ; Search time 45 Seconds
(without alignments)
477.682 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNGKNGYRGTSK.....TNSQVREYCKLPSCDSQSPV 260

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	100.0	260	2	US-09-982-516-1
2	1535	99.7	339	1	US-08-248-629A-3
3	1535	99.7	339	1	US-08-451-932-3
4	1535	99.7	339	1	US-08-452-260-3
5	1535	99.7	339	1	US-08-326-785-3
6	1535	99.7	339	1	US-08-612-788-3
7	1535	99.7	339	1	US-08-605-598B-3
8	1535	99.7	339	1	US-08-429-743-3
9	1535	99.7	339	1	US-08-866-735-3
10	1535	99.7	339	2	US-09-066-028-3
11	1535	99.7	339	2	US-09-335-325-3
12	1535	99.7	339	2	US-09-335-614-3
13	1535	99.7	339	4	PCR-US95-05107-3
14	1535	99.7	374	2	US-09-377-250-2
15	1535	99.7	375	2	US-09-377-250-2
16	1535	99.7	378	1	US-08-612-788-42
17	1535	99.7	378	2	US-09-066-028-42
18	1535	99.7	378	2	US-09-206-059-1
19	1535	99.7	378	2	US-09-335-325-42
20	1535	99.7	378	2	US-09-335-614-42
21	1535	99.7	451	2	US-09-377-250-1
22	1535	99.7	452	2	US-09-377-250-4
23	1535	99.7	790	1	US-08-469-486-54
24	1535	99.7	790	1	US-08-469-686-54
25	1535	99.7	791	1	US-08-643-219-1
26	1535	99.7	791	1	US-09-131-995-1
27	1535	99.7	791	1	US-08-832-087B-1

28	1535	99.7	791	2	US-08-851-350-1	Sequence 1, Appli
29	1535	99.7	791	2	US-09-132-154-1	Sequence 1, Appli
30	1535	99.7	791	2	US-08-991-761A-6	Sequence 6, Appli
31	1535	99.7	791	2	US-08-924-287A-1	Sequence 1, Appli
32	1535	99.7	791	2	US-10-360-101-257	Sequence 257, App
33	1535	99.7	810	1	US-07-854-603-2	Sequence 2, Appli
34	1535	99.7	810	1	US-08-147-000B-29	Sequence 29, Appli
35	1535	99.7	810	2	US-09-086-514-1	Sequence 1, Appli
36	1535	99.7	810	2	US-09-192-012-5	Sequence 5, Appli
37	1535	99.7	810	2	US-09-403-736-1	Sequence 1, Appli
38	1535	99.7	810	2	US-09-701-265-1	Sequence 1, Appli
39	1535	99.7	814	1	US-08-750-711-1	Sequence 1, Appli
40	1532	99.5	713	2	US-09-949-016-9983	Sequence 9983, Ap
41	1531	99.4	369	2	US-09-701-265-2	Sequence 2, Appli
42	1531	99.4	810	6	5200340-8	Patent No. 5200340
43	1511	98.1	352	1	US-08-612-788-40	Sequence 40, Appli
44	1511	98.1	352	2	US-09-066-028-40	Sequence 40, Appli
45	1511	98.1	352	2	US-09-335-325-40	Sequence 40, Appli

ALIGNMENTS

```
RESULT 1
US-09-982-516-1
; Sequence 1, Application US/09982516
; Patent No. 6723536
; GENERAL INFORMATION:
; APPLICANT: Madsen, John
; APPLICANT: Liang, Hong
; APPLICANT: Sim, Kim Lee
; APPLICANT: Zhou, Xinhua
; APPLICANT: Chang-Murad, Amy
; APPLICANT: Boerner, Renee J.
; APPLICANT: Bernerjo, Lourdes L.
; APPLICANT: Mistry, Filoz R.
; APPLICANT: Schrimsher, Jeffrey L.
; APPLICANT: Shepard, Scott R.
; TITLE OF INVENTION: Method of Producing and Purifying Angiotensin Protein
; FILE REFERENCE: 05213-0562 43170-264313
; CURRENT FILING DATE: 2002-09-10
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/32843
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 60/168,919
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-516-1

Query Match      100.0%; Score 1540; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.3e-139; Indels 0; Gaps 0;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTSKNGITTCQKWSSTSPHRFPSPATHPSEGLEENYCRNDN 60
DB 1 VYLSECKTGNGKNGYRGTSKNGITTCQKWSSTSPHRFPSPATHPSEGLEENYCRNDN 60

QY 61 DPGPWCCTTDPKRYDCDILCEBEGCMHSGENYDGKISKTSGLCQAMDSQSPHAY 120
DB 61 DPGPWCCTTDPKRYDCDILCEBEGCMHSGENYDGKISKTSGLCQAMDSQSPHAY 120

QY 121 GYISKPKNKULKKYCNCPDRELRPMWCFETDPNKRMELCIIPCTTTPSSGPTVOCLK 180
DB 121 GYISKPKNKULKKYCNCPDRELRPMWCFETDPNKRMELCIIPCTTTPSSGPTVOCLK 180

QY 181 GTGENYRGNVAVTYSGHTCQMSAQTPTHTERTPENPFCCKULDENYCNPDGKAPWCHT 240
DB 181 GTGENYRGNVAVTYSGHTCQMSAQTPTHTERTPENPFCCKULDENYCNPDGKAPWCHT 240
```

QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 2

US-08-248-629A-3
; Sequence 3, Application US/08248629A
; Patent No. 5639725

; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,629A
; FILING DATE: 04/26/94
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Scults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339
; TYPE: amino acid
; TOPOLOGY: linear

US-08-248-629A-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTNGKNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 120
DB 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 120
QY 121 GYIPSPFNKLNKKNYCRNPDRRLPWCFTTDPNKGWELCDIPRCTTPPSGPTYQCLK 180
DB 121 GYIPSPFNKLNKKNYCRNPDRRLPWCFTTDPNKGWELCDIPRCTTPPSGPTYQCLK 180
QY 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 3
US-08-451-932-3
; Sequence 3, Application US/08451932
; Patent No. 5733876

; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Method of Treating an Angiogenic
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,932
; FILING DATE: 05/26/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,629
; FILING DATE: 04/26/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Scults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339
; TYPE: amino acid
; TOPOLOGY: linear

US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
DB 1 VYLSECKTNGKNYRGTMSTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 120
DB 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLECOAMDOSPPAH 120
QY 121 GYIPSPFNKLNKKNYCRNPDRRLPWCFTTDPNKGWELCDIPRCTTPPSGPTYQCLK 180
DB 121 GYIPSPFNKLNKKNYCRNPDRRLPWCFTTDPNKGWELCDIPRCTTPPSGPTYQCLK 180
QY 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 4
US-08-452-260-3
; Sequence 3, Application US/08452260
; Patent No. 5776704
; GENERAL INFORMATION:

```

; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Method of Diagnosing an Angiogenic
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,260
; FILING DATE: 05/26/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,629
; FILING DATE: 04/26/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Stults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-452-260-3

Query Match          99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSEKTKNGKNYGTMSKTKNGITCQKMSSTSPHPRPSPATPSEGLSENYCNPN 60
DB 1 VLSSEKTKNGKNYGTMSKTKNGITCQKMSSTSPHPRPSPATPSEGLSENYCNPN 60
QY 61 DPGPWCYTTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAWDSQSPH 120
DB 61 DPGPWCYTTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAWDSQSPH 120
QY 121 GYIPSKFPKKNLKKNYCRNPDRBLRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 121 GYIPSKFPKKNLKKNYCRNPDRBLRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
QY 161 GGENYRGNAVAVTSGHCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGKRAPWC 240
DB 161 GGENYRGNAVAVTSGHCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGKRAPWC 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5
US-08-326-785-3
; Sequence 3, Application US/08326785
; Patent No. 5792845
; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;

```

```

; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,785
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,629
; FILING DATE: 04/26/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Stults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-326-785-3

Query Match          99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSEKTKNGKNYGTMSKTKNGITCQKMSSTSPHPRPSPATPSEGLSENYCNPN 60
DB 1 VLSSEKTKNGKNYGTMSKTKNGITCQKMSSTSPHPRPSPATPSEGLSENYCNPN 60
QY 61 DPGPWCYTTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAWDSQSPH 120
DB 61 DPGPWCYTTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAWDSQSPH 120
QY 121 GYIPSKFPKKNLKKNYCRNPDRBLRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 121 GYIPSKFPKKNLKKNYCRNPDRBLRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
QY 161 GGENYRGNAVAVTSGHCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGKRAPWC 240
DB 161 GGENYRGNAVAVTSGHCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGKRAPWC 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6
US-08-612-788-3
; Sequence 3, Application US/08612788
; Patent No. 5837682
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; APPLICANT: Cao, Yihai
; APPLICANT: Sim, B. Kim Lee
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
;

```

COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-612-788-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSGEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSGEGLEENYCRNPDN 60
QY 61 DPGPCYCTTDPKRYDYCDILECEBECMHCSGENYDGIKSKTMSGLECOAMDSQSPH 120
DB 61 DPGPCYCTTDPKRYDYCDILECEBECMHCSGENYDGIKSKTMSGLECOAMDSQSPH 120
QY 121 GYIPSKFPKNLKNYCRNPDRELRPWCFTTDPNKRWEICDIPRCTTPPSSGPTYOCLK 180
DB 121 GYIPSKFPKNLKNYCRNPDRELRPWCFTTDPNKRWEICDIPRCTTPPSSGPTYOCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGRAPMCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGRAPMCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7
US-08-605-598B-3
Sequence 3, Application US/08605598B
Patent No. 5863372
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Lin, Jie
APPLICANT: O'Reilly, Michael S.
TITLE OF INVENTION: Aggregate Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta

STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,598B
FILING DATE: 22-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Human Angiostatin
US-08-605-598B-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSGEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSGEGLEENYCRNPDN 60
QY 61 DPGPCYCTTDPKRYDYCDILECEBECMHCSGENYDGIKSKTMSGLECOAMDSQSPH 120
DB 61 DPGPCYCTTDPKRYDYCDILECEBECMHCSGENYDGIKSKTMSGLECOAMDSQSPH 120
QY 121 GYIPSKFPKNLKNYCRNPDRELRPWCFTTDPNKRWEICDIPRCTTPPSSGPTYOCLK 180
DB 121 GYIPSKFPKNLKNYCRNPDRELRPWCFTTDPNKRWEICDIPRCTTPPSSGPTYOCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGRAPMCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGRAPMCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8
US-08-429-743-3
Sequence 3, Application US/08429743
Patent No. 5885795
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
APPLICANT: Sim, Kim Lee
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769

```

1      COMPUTER READABLE FORM:
2      MEDIUM TYPE: Floppy disk
3      COMPUTER: IBM PC compatible
4      OPERATING SYSTEM: PC-DOS/MS-DOS
5      SOFTWARE: PatentIn Release #1.0, Version #1.30
6      CURRENT APPLICATION DATA:
7      APPLICATION NUMBER: US/08/429,743
8      FILING DATE:
9      CLASSIFICATION: 424
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: US 08/248,629
12     FILING DATE: 26-APR-1994
13     PRIOR APPLICATION DATA:
14     APPLICATION NUMBER: US 08/326,765
15     FILING DATE: 20-OCT-1994
16     ATTORNEY/AGENT INFORMATION:
17     NAME: Johnson, James D.
18     REGISTRATION NUMBER: 31,771
19     REFERENCE/DOCKET NUMBER: 05213-0122
20     TELECOMMUNICATION INFORMATION:
21     TELEPHONE: 404-818-3700
22     TELEFAX: 404-818-3799
23     INFORMATION FOR SEQ ID NO: 3:
24     SEQUENCE CHARACTERISTICS:
25     LENGTH: 339 amino acids
26     TYPE: amino acid
27     STRANDEDNESS:
28     TOPOLOGY: linear
29     MOLECULE TYPE: protein
30     HYPOTHETICAL: NO
31     ORIGINAL SOURCE:
32     ORGANISM: Homo sapiens
33     US-08-429-743-3

```

Query Match	99.7%	Score 1535	DB 1	Length 339
Best Local Similarity	99.6%	Pred. No. 1.4e-138		
Matches 259	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

QY	1	YLISLCKTNGNGNYGTMSKTNGITCOQWSSTPHPRPSPATHPSEGLSEENYCRNP	60
QY	1	YLISLCKTNGNGNYGTMSKTNGITCOQWSSTPHPRPSPATHPSEGLSEENYCRNP	60
Db	1	YLISLCKTNGNGNYGTMSKTNGITCOQWSSTPHPRPSPATHPSEGLSEENYCRNP	60
QY	61	DPOGWCYTTDPEKRYDCDILECEBECMHSGENYDGKISKTMSGLECAMDSQSPH	120
Db	61	DPOGWCYTTDPEKRYDCDILECEBECMHSGENYDGKISKTMSGLECAMDSQSPH	120
QY	121	GYIPKFPKKNLKNYCRNPDELRPWCCTTDPNKMWELCDIYRCTTTPPSSSPTQCK	180
Db	121	GYIPKFPKKNLKNYCRNPDELRPWCCTTDPNKMWELCDIYRCTTTPPSSSPTQCK	180
QY	181	GTGENYRGNAVATVTSGHTCOHNSAQPHHRTPEHPNFCNLIDENYCRNPDGGRAPWCHT	240
Db	181	GTGENYRGNAVATVTSGHTCOHNSAQPHHRTPEHPNFCNLIDENYCRNPDGGRAPWCHT	240
QY	241	TNSQVRWEYCKIPSCDSSPV 260	
Db	241	TNSQVRWEYCKIPSCDSSPV 260	

RESULT 9
US-08-866-735-3
: Sequence 3, Application US/08866735
: Patent No. 5845403
: GENERAL INFORMATION:
: APPLICANT: Folkman, M. Judah
: APPLICANT: O'Reilly, Michael
: TITLE OF INVENTION: Angiotensin Fragments and Method of Use
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Jones & Askew, LLP
: STREET: 191 Peachtree Street, 37th Floor
: CITY: Atlanta
: STATE: Georgia

```

1 COUNTRY: USA
2
3 ZIP: 30303-1769
4
5 COMPUTER READABLE FORM:
6
7 . MEDIUM TYPE: Floppy disk
8
9 . COMPUTER: IBM PC compatible
10
11 . OPERATING SYSTEM: PC-DOS/MS-DOS
12
13 . SOFTWARE: Patentin Release #1.0, Ver
14
15 . CURRENT APPLICATION DATA:
16
17 . APPLICATION NUMBER: US/08/866,735
18
19 . FILING DATE: 30-MAY-1997
20
21 CLASSIFICATION: 435
22
23 ATTORNEY/AGENT INFORMATION:
24
25 . NAME: Warren, William L.
26
27 . REGISTRATION NUMBER: 36,714
28
29 . REFERENCE/DOCKET NUMBER: 0540-01229
30
31 . TELECOMMUNICATION INFORMATION:
32
33 . TELEPHONE: (404) 818-3700
34
35 . TELEFAX: (404) 818-3799
36
37 . INFORMATION FOR SEQ ID NO: 3:
38
39 . SEQUENCE CHARACTERISTICS:
40
41 . LENGTH: 339 amino acids
42
43 . TYPE: amino acid
44
45 . STRANDEDNESS:
46
47 . TOPOLOGY: linear
48
49 . MOLECULE TYPE: protein
50
51 . HYPOTHETICAL: NO
52
53 . ANTI-SENSE: NO
54
55 . FRAGMENT TYPE: N-terminal
56
57 . ORIGINAL SOURCE:
58
59 . ORGANISM: Homo sapiens
60
61 . IMMEDIATE SOURCE:
62
63 . CLONE: Angiotensin fragment
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978

```

Query Match	99.7%	Score 1535;	DB 1;	Length 339;
Best Local Similarity	99.6%	Pred. No. 1.4e-138;		
Matches 259; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	VYLSEKTKNGKNGYGTMSKTKNGGTLCOKMSSTSPHRRPSPATHPSGAELENNCRAPDN	60
Db	1	VYLSEKTKNGKNGYGTMSKTKNGGTLCOKMSSTSPHRRPSPATHPSGAELENNCRAPDN	60
Qy	61	DPQSPCYTTTDEPKRYDCDILACEBOMHSGENYDGKISKMSGLEQAMDSQSPHAI	120
Db	61	DPQSPCYTTTDEPKRYDCDILACEBOMHSGENYDGKISKMSGLEQAMDSQSPHAI	120
Qy	121	GTPSPKPNKKNKRYCNRPDRELPMCFPTTDPNKRMLCDIPCTTTPPSGGTYQCLK	180
Db	121	GTPSPKPNKKNKRYCNRPDRELPMCFPTTDPNKRMLCDIPCTTTPPSGGTYQCLK	180
Qy	181	GTGENYRGVAVATVSGHCOHWSAQTPTHTERTPENFPCKULDENYCRNPDGKAPWCHT	240
Db	181	GTGENYRGVAVATVSGHCOHWSAQTPTHTERTPENFPCKULDENYCRNPDGKAPWCHT	240
Qy	241	TNSQVAMEYCKIPSCDSSFPV	260
Db	241	TNSQVAMEYCKIPSCDSSFPV	260

RESULT 10
US-09-066-028-3
Sequence 3, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marten, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiotensin fragment
US-09-066-028-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSPBGLSENYCRNPDN 60
DB 1 VLSSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSPBGLSENYCRNPDN 60
QY 61 DPGFPCYTTDDPEKRYDYCDILECEBECMHGSGENTDGIKISKTMSGLBQAMDSQSPHAF 120
DB 61 DPGFPCYTTDDPEKRYDYCDILECEBECMHGSGENTDGIKISKTMSGLBQAMDSQSPHAF 120
QY 121 GYIPSKFPKNLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
DB 121 GYIPSKFPKNLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLBENTCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLBENTCRNPDGKRAPWCHT 240
QY 241 TNSQVRMEYCKIPSCDSSPV 260
DB 241 TNSQVRMEYCKIPSCDSSPV 260

RESULT 11
US-09-335-325-3
Sequence 3, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Michael
Cao, Yihai
Sim, B. Kim Lee

TITLE OF INVENTION: Angiotensin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Arkew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marten, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiotensin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSPBGLSENYCRNPDN 60
DB 1 VLSSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPSPATPSPBGLSENYCRNPDN 60
QY 61 DPGFPCYTTDDPEKRYDYCDILECEBECMHGSGENTDGIKISKTMSGLBQAMDSQSPHAF 120
DB 61 DPGFPCYTTDDPEKRYDYCDILECEBECMHGSGENTDGIKISKTMSGLBQAMDSQSPHAF 120
QY 121 GYIPSKFPKNLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
DB 121 GYIPSKFPKNLKKNYCRNPDRELPRWCFTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLBENTCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLBENTCRNPDGKRAPWCHT 240
QY 241 TNSQVRMEYCKIPSCDSSPV 260
DB 241 TNSQVRMEYCKIPSCDSSPV 260

RESULT 12
US-09-335-614-3
Sequence 3, Application US/09335614

Db 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 14
US-09-377-250-3
; Sequence 3, Application US/09377250
; Patent No. 6365364
; GENERAL INFORMATION:
; APPLICANT: MANN, KENNETH G.
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
; FILE REFERENCE: 48409/360
; CURRENT APPLICATION NUMBER: US/09/377,250
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiogenesis inhibitor
; NAME/KEY: MOD RES
; LOCATION: (264)
; OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-3

Query Match 99.7%; Score 1535; DB 2; Length 374;
Best Local Similarity 99.6%; Pred. No. 1.6e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTLSECKTGNGKNGYGTMSKTNGITGCKWSSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
Db 1 VTLSECKTGNGKNGYGTMSKTNGITGCKWSSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
QY 61 DPGFWCYTTDPBKRKYDYCDILBCEBECMHCSEGENYDGKISKTMGLEGQAADSQSPHAA 120
Db 61 DPGFWCYTTDPBKRKYDYCDILBCEBECMHCSEGENYDGKISKTMGLEGQAADSQSPHAA 120
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
QY 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
Db 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVMEYCKIPSCDSSPV 260
Db 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 15
US-09-377-250-2
; Sequence 2, Application US/09377250
; Patent No. 6365364
; GENERAL INFORMATION:
; APPLICANT: MANN, KENNETH G.
; APPLICANT: SWORDS JENNY, NANCY
; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
; FILE REFERENCE: 48409/360
; CURRENT APPLICATION NUMBER: US/09/377,250
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiogenesis inhibitor

; NAME/KEY: MOD RES
; LOCATION: (265)
; OTHER INFORMATION: Xaa = Gln or Glu
US-09-377-250-2

Query Match 99.7%; Score 1535; DB 2; Length 375;
Best Local Similarity 99.6%; Pred. No. 1.6e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTLSECKTGNGKNGYGTMSKTNGITGCKWSSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
Db 2 VTLSECKTGNGKNGYGTMSKTNGITGCKWSSSTSPHPRPSPATHPSEGLEENYCRNPDN 61
QY 61 DPGFWCYTTDPBKRKYDYCDILBCEBECMHCSEGENYDGKISKTMGLEGQAADSQSPHAA 120
Db 61 DPGFWCYTTDPBKRKYDYCDILBCEBECMHCSEGENYDGKISKTMGLEGQAADSQSPHAA 121
QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 181
QY 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
Db 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 241
QY 241 TNSQVMEYCKIPSCDSSPV 260
Db 241 TNSQVMEYCKIPSCDSSPV 261

Search completed: January 25, 2006, 17:11:54
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 16:54:09 ; Search time 137 Seconds
(without alignments)
833.858 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540
Sequence: 1 VYLSECKTGNKYNRTGWSK.....TNSQVREYCKIPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.21:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*
9: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1540	100.0	260	3	AA026486 Deglycosy
2	1540	100.0	260	4	AAU01209 Human Ang
3	1537	99.8	869	7	ADK40316 C-termina
4	1537	99.8	869	7	ADK40314 C-termina
5	1535	99.7	260	6	AA079748 Human pla
6	1535	99.7	268	2	AA02109 A multifu
7	1535	99.7	285	2	AA02102 A multifu
8	1535	99.7	339	2	AA083961 Human pla
9	1535	99.7	339	2	AA07581 N-Termina
10	1535	99.7	339	2	AA094038 Human ang
11	1535	99.7	339	4	AA050518 Human ang
12	1535	99.7	339	7	ADG47024 Human ang
13	1535	99.7	339	8	ADM11543 Human pla
14	1535	99.7	363	3	AA070255 Human ang
15	1535	99.7	364	2	AA0702106 A multifu
16	1535	99.7	374	3	AA079226 Angiogene
17	1535	99.7	375	3	AA079225 Angiogene
18	1535	99.7	378	2	AA075729 Human kri
19	1535	99.7	378	3	AA016450 Human ang
20	1535	99.7	378	5	AA048894 Human ang
21	1535	99.7	378	7	ADG47063 Human kri
22	1535	99.7	381	2	AA02105 A multifu
23	1535	99.7	381	2	AA02101 A multifu
24	1535	99.7	391	6	ADA08454 Mammalian

25	1535	99.7	391	8	ADP67426 A61 anti-
26	1535	99.7	394	6	ADA08455 Mammalian
27	1535	99.7	394	6	ADP67427 A61 anti-
28	1535	99.7	452	3	AA079224 Angiogene
29	1535	99.7	453	2	AA02093 A multifu
30	1535	99.7	453	2	AA02099 A multifu
31	1535	99.7	453	2	AA02095 A multifu
32	1535	99.7	453	2	AA02096 A multifu
33	1535	99.7	453	2	AA095051 Amino aci
34	1535	99.7	470	2	AA02112 A multifu
35	1535	99.7	480	7	ABU64288 Human ang
36	1535	99.7	484	6	AA079749 Human pla
37	1535	99.7	563	5	AB075942 Endotheli
38	1535	99.7	566	2	AA02100 A multifu
39	1535	99.7	571	5	AB075944 Angiotens
40	1535	99.7	576	5	AB075943 Angiotens
41	1535	99.7	579	8	ADG82532 Proactin
42	1535	99.7	654	8	ABM83810 Human dia
43	1535	99.7	672	8	ABM83809 Human dia
44	1535	99.7	714	7	ABG75025 Lys-plasm
45	1535	99.7	790	2	AA060519 Human 'G1

ALIGNMENTS

RESULT 1	AA026486	standard; protein; 260 AA.
ID	AA026486	
AC	AA026486;	
DT	16-JAN-2001	(first entry)
DE	Deglycosylated kringle 1-5 region protein.	
KW	Deglycosylated; kringle; angiogenesis; human.	
OS	Homo sapiens.	
PN	WO20047729-A1.	
XX	17-AUG-2000.	
PF	10-FEB-2000; 2000WO-US003482.	
PR	10-FEB-1999; 99US-0119562P.	
PR	07-APR-1999; 99US-0128062P.	
XX	(ENTR-) EXTREMED INC.	
XX	(CHIL-) CHILDRENS MEDICAL CENT.	
XX	Petrie-Shepherd S, Folkman MJ, Liang H, Macdonald NJ, Sim KL;	
XX	WPI: 2000-579032/54.	
XX	N-PSDB; AAA94906.	
XX	Novel composition comprising deglycosylated fragments of kringle 1-5	
XX	regions of plasminogen linked to the glycosylated form, useful for	
XX	inhibiting angiogenesis.	
XX	Claim 7; Fig 1; 42pp; English.	
XX	The present sequence is deglycosylated kringle 1-5 region protein.	
XX	Deglycosylated kringle 1-5 region protein has increased antiangiogenic	
XX	activity as compared to glycosylated kringle 1-5 region protein. The	
XX	deglycosylated kringle 1-5 region protein was isolated from human	
XX	plasminogen by affinity chromatography	
XX	Sequence 260 AA;	
XX	Query Match	100.0%; Score 1540; DB 3; Length 260;
XX	Best Local Similarity	100.0%; Pred. No. 1e-90;

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRGTGMSKTNGITCOKMSTSPHRRPSPATHPSEGLSENYCRNPDN 60
 DB 1 VYLSECKTGNGKNGRGTGMSKTNGITCOKMSTSPHRRPSPATHPSEGLSENYCRNPDN 60
 QY 61 DPQGPWCYTTDPEKRYDCDILCEBECCHMGSGENYDKISKMSGLECOAMDOSPHAH 120
 DB 61 DPQGPWCYTTDPEKRYDCDILCEBECCHMGSGENYDKISKMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNNKLNKKNYCRNPDRELPMWCFITDPMKRWELCDIPRCTPPSSGPTYQCLK 180
 DB 121 GYIPSKFPNNKLNKKNYCRNPDRELPMWCFITDPMKRWELCDIPRCTPPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 2

AAU01209
 ID AAU01209 standard; protein; 260 AA.
 XX AC AAU01209;
 XX DT 26-SEP-2001 (first entry)
 XX DE Human Angiostatin (hASv3) protein.
 XX KW Human: Angiostatin; recombinant production; cation exchange column;
 KW fermentation; angiogenesis mediated disease; leukaemia; tumour;
 KW rheumatoid arthritis; plaque neovascularisation.
 XX OS Homo sapiens.
 XX PN WO200140260-A2.
 XX PD 07-JUN-2001.
 XX PF 04-DEC-2000; 2000WO-US032843.
 XX PR 03-DEC-1999; 99US-0168919P.
 XX PA (ENTR-) ENTREMED INC.
 XX PI Madesen J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ,
 PI Bermejo LL, Mistry FR, Schrimsher JL, Shepard SR;
 XX WPI; 2001-408277/43.
 DR N-PSDB; AAS04181.
 XX PT Purifying recombinant angiostatin, involves applying fermented broth
 PT containing angiostatin to expanded bed cation exchange column, anion
 PT exchange column, hydroxyapatite column, hydrophobic column and a
 PT membrane.
 XX Example 1; Page 22; 49p; English.
 CC The present sequence representing Angiostatin protein is given in an
 CC invention providing a method for recombinant production, recovery and
 CC purification of Angiostatin protein. Purification of recombinant
 CC Angiostatin comprises applying crude fermentation broth containing the
 CC protein to an expanded bed cation exchange column, eluting it, and
 CC applying the eluate to anion exchange column, repeating the process of
 CC eluting and applying, to hydroxyapatite column, hydrophobic column and
 CC membrane, in order, and collecting fluid passing through the membrane.
 CC Angiostatin is useful for treating angiogenesis mediated diseases,
 CC including solid tumours, leukaemia, tumour metastases, benign tumours,
 CC rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Osler-Webber

CC syndrome, myocardial angiogenesis, plaque neovascularisation,
 CC telangiectasia, haemophilic joints, angiodioma and wound granulation.
 CC As a centrifugation technique is not employed in the process, damage to
 CC the cells with concomitant release of undesirable biological materials
 CC such as cytochromes, pigments, enzymes, chemicals and other undesirable
 CC cellular constituents and debris, is prevented. Large scale recovery and
 CC purification of proteins is greater than that obtained from prior art
 CC methods. Active Angiostatin can be stored in buffers for extended periods
 CC of time, in vials or other containers, either in solution which may be
 CC liquid or frozen, or lyophilised
 XX Sequence 260 AA;

Query Match 100.0%; Score 1540; DB 4; Length 260;

Best Local Similarity 100.0%; Pred. No. 1e-90;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRGTGMSKTNGITCOKMSTSPHRRPSPATHPSEGLSENYCRNPDN 60
 DB 1 VYLSECKTGNGKNGRGTGMSKTNGITCOKMSTSPHRRPSPATHPSEGLSENYCRNPDN 60
 QY 61 DPQGPWCYTTDPEKRYDCDILCEBECCHMGSGENYDKISKMSGLECOAMDOSPHAH 120
 DB 61 DPQGPWCYTTDPEKRYDCDILCEBECCHMGSGENYDKISKMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNNKLNKKNYCRNPDRELPMWCFITDPMKRWELCDIPRCTPPSSGPTYQCLK 180
 DB 121 GYIPSKFPNNKLNKKNYCRNPDRELPMWCFITDPMKRWELCDIPRCTPPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 3

ADK40316
 ID ADK40316 standard; protein; 869 AA.
 XX AC ADK40316;
 XX DT 06-MAY-2004 (first entry)
 XX DE C-terminal albumin-angiostatin fusion protein.
 XX KW cytostatic; vaccine; albumin fusion protein;
 KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
 KW collagen.
 XX OS Homo sapiens.
 XX PN WO2003066085-A1.
 XX PD 14-AUG-2003.
 XX PF 07-FEB-2003; 2003WO-IB000433.
 XX PR 07-FEB-2002; 2002US-0355547P.
 XX PA (AVRT) AVENTIS BEHRING GMBH.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PI Mertine P, Celik I, Kisker O, Sleep D, Hay J, Hauser H,
 DR WPI; 2003-731479/69.
 DR N-PSDB; ADK40315.
 XX PT New albumin fusion protein comprising an angiogenesis inhibiting peptide
 PT and an albumin having an albumin activity, or their fragments or

PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
XX
PS Disclosure; Fig 8; 136pp; English.
XX
CC The invention relates to an albumin fusion protein comprising an
CC angiogenesis inhibiting peptide and an albumin having an albumin
CC activity, or their fragments or variants. The albumin fusion proteins,
CC compositions, vaccines and methods are useful for treating angiogenesis-
CC dependent tumor, e.g. cancer. This sequence represents an C-terminal
CC albumin-angiotensin fusion protein.
XX
SQ Sequence 869 AA;
XX
Query Match 99.8%; Score 1537; DB 7; Length 869;
Best Local Similarity 99.6%; Pred. No. 4.9e-90;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
DB 610 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPRFSPATHPSEGLEENYCRNPDN 669
QY 61 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLECOAMDSPRAH 120
DB 670 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLECOAMDSPRAH 729
QY 121 GYIPSKFPKNLKKNYCNRNPRELRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYQCLK 180
DB 730 GYIPSKFPKNLKKNYCNRNPRELRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYQCLK 789
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 790 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 849
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 850 TNSQVRWEYCKIPSCDSSPV 869
XX
RESULT 4
ADK40314
ID ADK40314 standard; protein; 869 AA.
XX
AC ADK40314;
XX
DT 06-MAY-2004 (first entry)
XX
DE N-terminal angiotensin-albumin fusion protein.
XX
KM cyostatic; vaccine; albumin fusion protein;
KM angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
KM collagen.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003066085-A1.
XX
PD 14-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-1B000433.
XX
PR 07-FEB-2002; 2002US-0355547P.
XX
PA (AVENTIS BEHRING GMBH.
PA (DELTA) DELTA BIOTECHNOLOGY LTD.
XX
PI Mertins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
XX
DR WPI; 2003-731479/69.
XX
DR N-PSDB; ADK40313.
XX
PT New albumin fusion protein comprising an angiogenesis inhibiting peptide
PT and an albumin having an albumin activity, or their fragments or

PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
XX
PS Disclosure; Fig 6; 136pp; English.
XX
CC The invention relates to an albumin fusion protein comprising an
CC angiogenesis inhibiting peptide and an albumin having an albumin
CC activity, or their fragments or variants. The albumin fusion proteins,
CC compositions, vaccines and methods are useful for treating angiogenesis-
CC dependent tumor, e.g. cancer. This sequence represents an N-terminal
CC angiotensin-albumin fusion protein.
XX
SQ Sequence 869 AA;
XX
Query Match 99.8%; Score 1537; DB 7; Length 869;
Best Local Similarity 99.6%; Pred. No. 4.9e-90;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
DB 25 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRPRFSPATHPSEGLEENYCRNPDN 84
QY 61 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLECOAMDSPRAH 120
DB 85 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLECOAMDSPRAH 144
QY 121 GYIPSKFPKNLKKNYCNRNPRELRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYQCLK 180
DB 145 GYIPSKFPKNLKKNYCNRNPRELRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYQCLK 204
QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 205 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 264
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 265 TNSQVRWEYCKIPSCDSSPV 284
XX
RESULT 5
AAG79748
ID AAG79748 standard; protein; 260 AA.
XX
AC AAG79748;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human plasma/ogen kring/le domains 1-3, K1-3.
XX
KM Human; plasminogen; angiotensin; neovascularisation; kring/le domain;
KM cell proliferation; viral vector; replication-defective; cancer; tumour.
XX
OS Homo sapiens.
OS
XX
PN WO200288173-A2.
XX
PD 07-NOV-2002.
XX
PF 29-APR-2002; 2002WO-US013461.
XX
PR 30-APR-2001; 2001US-028673P.
XX
PR 05-APR-2002; 2002US-0370634P.
XX
PA (CELL-) CELL GENESYS INC.
XX
PI Chang B, Wu W, Macarthur J, Patel S, Jooss K, Mendez M;
XX
DR WPI; 2003-129131/12.
XX
DR N-PSDB; ABA00776.
XX
PT New recombinant viral vector expressing human angiotensin useful for
PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.
XX
PS Disclosure; Page 75-76; 83pp; English.

XX This sequence represents kringle domains 1-3 of human plasminogen. A 38
 CC KD-N-terminal fragment of plasminogen is referred to as angiotensin and
 CC inhibits neovascularization. Angiotensin contains 4 kringle domains of
 CC the parent molecule. However, angiotensin containing all 4 kringle
 CC domains (K1-4) was found to be no more potent as an inhibitor of cell
 CC proliferation than an angiotensin only containing K1-3. Therefore,
 CC kringle 4 does not possess inhibitory activity. A fragment of the
 CC plasminogen coding sequence may be used in the recombinant viral vector
 CC of the invention for obtaining angiotensin activity. The vector comprises
 CC a promoter capable of expressing human angiotensin operably linked to a
 CC structural gene encoding one or more domains of human angiotensin. The
 CC vector, which may be a replication-defective viral vector, is useful for
 CC inhibiting angiogenesis in a mammal, especially with cancer or a tumor

XX Sequence 260 AA;

Query Match 99.7%; Score 1535; DB 6; Length 260;
 Best Local Similarity 99.6%; Pred. No. 2.1e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
 DB 1 VYLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
 QY 61 DPGGWCCTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLBQAWDSQSPHAA 120
 DB 61 DPGGWCCTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLBQAWDSQSPHAA 120
 QY 121 GYIPSKFPMKNLKNKNCNRPDLRLPWCFTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
 DB 121 GYIPSKFPMKNLKNKNCNRPDLRLPWCFTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPFCNKLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPFCNKLDENYCRNPDGRAPWCHT 240
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6
 ID AAY02109 standard; protein; 268 AA.

XX AAY02109;

DT 16-JUL-1999 (first entry)

DE A multifunctional protein of the invention.

XX Angiotensin; endostatin; interferon; thrombospondin;
 KM interferon-inducible protein; platelet factor 4; anti-angiogenic;
 KM anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;
 KM diabetic retinopathy; macular degeneration; arthritis;
 KM tumor cell production.

XX Synthetic.

OS Homo sapiens.

XX WO9916889-A1.

XX 08-APR-1999.

PF 30-SEP-1998; 98WO-US020464.

PR 01-OCT-1997; 97US-0060609P.

PA (SEAR) SEARLE & CO G D.

PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;
 McKearn JP;

XX WPI; 1999-255098/21.
 XX New multifunctional proteins useful for treating angiogenic-mediated
 PT diseases.

PS Claim 5; Page 104; 121pp; English.

XX The specification describes multifunctional proteins which comprise
 CC combinations of angiotensin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have anti-
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may
 CC exhibit useful properties such as having similar or greater biological
 CC activity when compared to a single factor or by having improved half-life
 CC or decreased adverse side effects, or a combination of these properties.
 CC The proteins can be used for treating an angiogenic-mediated disease,
 CC e.g., cancer, diabetic retinopathy, macular degeneration, or arthritis.
 CC They can also be used for inhibiting the production of tumor cells
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
 CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
 CC in a patient and for inhibiting tumor growth. The present sequence
 CC represents a multifunctional protein of the invention

XX Sequence 268 AA;

Query Match 99.7%; Score 1535; DB 2; Length 268;
 Best Local Similarity 99.6%; Pred. No. 2.2e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 60
 DB 3 VYLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPDN 62
 QY 61 DPGGWCCTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLBQAWDSQSPHAA 120
 DB 63 DPGGWCCTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLBQAWDSQSPHAA 122
 QY 121 GYIPSKFPMKNLKNKNCNRPDLRLPWCFTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
 DB 123 GYIPSKFPMKNLKNKNCNRPDLRLPWCFTTDPNKNMELCDIPRCTPPSSGPTYQCLK 182
 QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPFCNKLDENYCRNPDGRAPWCHT 240
 DB 183 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPFCNKLDENYCRNPDGRAPWCHT 242
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 243 TNSQVRWEYCKIPSCDSSPV 262

RESULT 7

ID AAY02102 standard; protein; 285 AA.

XX AAY02102;

DT 16-JUL-1999 (first entry)

DE A multifunctional protein of the invention.

XX Angiotensin; endostatin; interferon; thrombospondin;
 KM interferon-inducible protein; platelet factor 4; anti-angiogenic;
 KM anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;
 KM diabetic retinopathy; macular degeneration; arthritis;
 KM tumor cell production.

XX Synthetic.

OS Homo sapiens.

XX WO9916889-A1.

XX 08-APR-1999.

PF 30-SEP-1998; 98WO-US020464.
 XX
 PR 01-OCT-1997; 97US-0060609P.
 XX
 PA (SEARL) SEARLE & CO G D.
 XX
 PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK,
 PI McKearn JP;
 DR WPI, 1999-255098/21.
 XX
 PT New multifunctional proteins useful for treating angiogenic-mediated
 PT diseases.
 XX
 PS Claim 5; Page 97-98; 121pp; English.
 XX
 CC The specification describes multifunctional proteins which comprise
 CC combinations of angiotensin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have anti-
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may
 CC exhibit useful properties such as having similar or greater biological
 CC activity when compared to a single factor or by having improved half-life
 CC or decreased adverse side effects, or a combination of these properties.
 CC The proteins can be used for treating an angiogenic-mediated disease,
 CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
 CC They can also be used for inhibiting the production of tumor cells
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
 CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
 CC in a patient and for inhibiting tumor growth. The present sequence
 CC represents a multifunctional protein of the invention
 XX
 SQ Sequence 285 AA;

Query Match 99.7%; Score 1535; DB 2; Length 285;
 Best Local Similarity 99.6%; Pred. No. 2.3e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGKMTSKTNGITCQKWSSTPHRRPSPATPSBGLBNYCRNDN 60
 DB 20 VYLSECKTGNKNGKMTSKTNGITCQKWSSTPHRRPSPATPSBGLBNYCRNDN 79
 QY 61 DPGPWCTTDPBKRKYDCDILECEBECMHSGENYDGIKSTWSGLECOAMDSPRAH 120
 DB 80 DPGPWCTTDPBKRKYDCDILECEBECMHSGENYDGIKSTWSGLECOAMDSPRAH 139
 QY 121 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTPPSSGPTYOCLK 180
 DB 140 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTPPSSGPTYOCLK 199
 QY 181 GTGENYRGNAVAVTYSGHTCOHWSAQTPTHTERTENPFCCKLIDENYCNPDGKAPWCHT 240
 DB 200 GTGENYRGNAVAVTYSGHTCOHWSAQTPTHTERTENPFCCKLIDENYCNPDGKAPWCHT 259
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 260 TNSQVRWEYCKIPSCDSSPV 279

RESULT 8
 AAR83961
 ID AAR83961 standard; protein; 339 AA.
 XX
 AC AAR83961;
 XX
 DT 10-MAR-1996 (first entry)
 XX
 DE Human plasminogen peptide fragment.
 XX
 KW Angiostatin; plasminogen; endothelial inhibitor; therapeutic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX

PN W09529242-A1.
 XX
 PD 02-NOV-1995.
 XX
 XX 26-APR-1995; 95WO-US005107.
 PF
 XX 26-APR-1994; 94US-00248629.
 PR 20-OCT-1994; 94US-00326785.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI O'Reilly MS, Folkman MW, Sim KL, Cao Y;
 PI WPI, 1995-382990/49.
 DR
 XX
 PT Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated
 PT disease esp. angiogenesis and cancer.
 XX
 PS Claim 4; Page 81-82; 108pp; English.

CC The sequence represents a plasminogen fragment which is compared with the
 CC corresponding plasminogen fragments of monkey (AAR83962), pig (AAR83963)
 CC and cattle (AAR83964) origin (in Fig.2), as well as the with the first
 CC 339 amino acids of mouse angiotensin (AAR83960) (i.e. aa's 98-436 of the
 CC complete 812 aa plasminogen molecule AAR83959). Human angiotensin is a
 CC plasminogen fragment starting at aa 97 or 99 of the complete plasminogen
 CC molecule. Angiotensin is an endothelial inhibitor, which reversibly
 CC inhibits proliferation of endothelial cells and thereby inhibits
 CC angiogenesis. It is useful in the treatment of a human or animal with
 CC angiogenic mediated disease e.g. arthritis, macular degeneration,
 CC diabetic retinopathy or cancer. Cells comprising angiotensin-coding
 CC sequences are useful for gene therapy of primary tumors
 XX
 SQ Sequence 339 AA;

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 2.7e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGKMTSKTNGITCQKWSSTPHRRPSPATPSBGLBNYCRNDN 60
 DB 1 VYLSECKTGNKNGKMTSKTNGITCQKWSSTPHRRPSPATPSBGLBNYCRNDN 60
 QY 61 DPGPWCTTDPBKRKYDCDILECEBECMHSGENYDGIKSTWSGLECOAMDSPRAH 120
 DB 61 DPGPWCTTDPBKRKYDCDILECEBECMHSGENYDGIKSTWSGLECOAMDSPRAH 120
 QY 121 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTPPSSGPTYOCLK 180
 DB 121 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTPPSSGPTYOCLK 180
 QY 181 GTGENYRGNAVAVTYSGHTCOHWSAQTPTHTERTENPFCCKLIDENYCNPDGKAPWCHT 240
 DB 181 GTGENYRGNAVAVTYSGHTCOHWSAQTPTHTERTENPFCCKLIDENYCNPDGKAPWCHT 240
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9
 AAW07581
 ID AAW07581 standard; protein; 339 AA.
 XX
 AC AAW07581;
 XX
 DT 24-JUN-1997 (first entry)
 XX
 DE N-Terminal angiotensin fragment.
 XX
 KW angiotensin; plasminogen; kringles; angiogenesis; cancer; arthritis;
 KW macular degeneration; diabetic retinopathy.
 XX

QY 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLEGCQAMDSOPH 120
 DB 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLEGCQAMDSOPH 120
 QY 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKMELCDIPRCTTTPSSGPTYQCLK 180
 DB 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKMELCDIPRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGVAVTVSGHTCQHWSAQTPTHHTPENPCKNLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGVAVTVSGHTCQHWSAQTPTHHTPENPCKNLDENYCRNPDGRAPWCHT 240
 QY 241 TNSOVRMEYCKIIPSCDSSPV 260
 DB 241 TNSOVRMEYCKIIPSCDSSPV 260

RESULT 11
 AAM50518
 ID AAM50518 standard; protein; 339 AA.
 AC AAM50518;
 DT 12-MAR-2002 (first entry)
 XX
 DE Human angiostatin.
 KW Angiostatin; plasminogen; human; angiogenesis; endothelial cell;
 KW cell proliferation; inhibitor; tumour; antiproliferative; cytostatic;
 KW vasotropic; antitumour; dermatological; antiinflammatory; antidiabetic;
 KW antineumatic; antiarthritic; ophthalmological; vulnery; anticancer;
 KW antibacterial; antiatherosclerotic; gynaecological; antipretic;
 KW cardiant; contraceptive; therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 6..255
 FT /label= Kringle-1-3
 FT Region 6..165
 FT /label= Kringle-1-2
 FT Region 6..84
 FT /label= Kringle-1
 FT Region 88..255
 FT /label= Kringle-2-3
 FT Region 88..165
 FT /label= Kringle-2
 FT Region 178..255
 FT /label= Kringle-3
 XX
 PN US2001029246-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 16-FEB-2001; 2001US-00788142.
 XX
 PR 30-MAY-1997; 97US-00866735.
 PR 24-APR-1998; 98US-00066028.
 PR 11-MAY-1999; 99US-00309821.
 PR 22-JUN-1999; 99US-00338387.
 XX
 PA (ORF/) O'REILLY M S.
 PA (FOK/) FOLKMAN M J.
 PA (CAO/) CAO Y.
 XX
 PI O'reilly MS, Folkman MJ, Cao Y;
 XX
 DR MPI; 2001-647990/74.
 XX
 PT Inhibiting endothelial cell proliferation, useful for treating angiogenic
 PT mediated diseases such as cancer, arthritis, comprises administering
 PT plasminogen fragment corresponding to kringle structures of plasminogen
 PT molecule.

XX
 PS Example 27; Fig 2A-C; 70pp; English.
 XX
 CC The present sequence is that of human angiostatin. A claimed method of
 CC inhibiting endothelial cell proliferation involves administering a
 CC plasminogen fragment (PF) having an amino acid sequence similar to the
 CC kringle 1-5 region of a plasminogen molecule. This includes a protein,
 CC termed angiostatin, defined by its ability to overcome the angiogenic
 CC activity of endogenous growth factors and by its amino acid sequence
 CC homology and structural similarity to an internal portion of plasminogen,
 CC beginning at approximately amino acid 98. The PF is preferably derived
 CC from mouse, human, Rhesus monkey, pig or cattle (see AAM50516-21). It is
 CC used in methods and compositions for the treatment of an angiogenic-
 CC mediated disease, including haemangioma, solid tumours, blood-borne
 CC tumours, leukaemia, metastasis, telangiectasia, psoriasis,
 CC atherosclerosis, scleroderma, pyogenic granuloma, myocardial
 CC angiogenesis, Crohn's disease, plaque neovascularisation, coronary
 CC collateral, cerebral laterals, arteriovenous malformations, ischaemic
 CC limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma,
 CC diabetic retinopathy, corneal graft rejection, retrolental fibroplasia,
 CC haemophilic joints, rheumatoid arthritis, diabetic neovascularisation,
 CC Osler-Webber syndrome, macular degeneration, wound healing, peptic ulcer,
 CC Helicobacter pylori related diseases, fractures, keloids, vasculogenesis,
 CC haematopoiesis, ovulation, menstruation, placental and cat scratch
 CC fever. Angiostatin is also useful as a birth control agent by preventing
 CC vascularisation required for embryo implantation. The compositions are
 CC particularly useful for treating or repressing the growth of tumours.
 CC Administration of angiostatin to a human or animal with prevascularised
 CC metastasized tumours will prevent the growth or expansion of those
 CC tumours. Gene therapy methods are also included in the invention
 XX

SO Sequence 339 AA;
 Query Match 99.7%; Score 1535; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 2.7e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTLSECKTGNKNGVGTMSKTNGITCQKWSSTSPRRPSPATPSSBGLSENYCNP 60
 DB 1 VTLSECKTGNKNGVGTMSKTNGITCQKWSSTSPRRPSPATPSSBGLSENYCNP 60
 QY 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLEGCQAMDSOPH 120
 DB 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLEGCQAMDSOPH 120
 QY 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKMELCDIPRCTTTPSSGPTYQCLK 180
 DB 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKMELCDIPRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGVAVTVSGHTCQHWSAQTPTHHTPENPCKNLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGVAVTVSGHTCQHWSAQTPTHHTPENPCKNLDENYCRNPDGRAPWCHT 240
 QY 241 TNSOVRMEYCKIIPSCDSSPV 260
 DB 241 TNSOVRMEYCKIIPSCDSSPV 260

RESULT 12
 ADG47024
 ID ADG47024 standard; protein; 339 AA.
 AC ADG47024;
 DT 11-MAR-2004 (first entry)
 XX
 DE Human angiostatin protein.
 XX
 KW Angiostatin; cell proliferation; angiogenic-mediated disease; cancer;
 KW arthritis; macular degeneration; diabetic retinopathy; psoriasis;
 KW scleroderma; Crohn's disease; wounds; peptic ulcer; fracture;
 KW gene therapy; plasminogen; cytostatic; ophthalmological; dermatological;
 KW antiinflammatory; vulnery; human.


```

DB 1 VYLSECKTNGKNYGTMSKTNGITCOQWMSSTSPHRRPSPATHPSEGLSENYCRNPDN 60
QY 61 DPOGWCCTTDBPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLEQAWDSOPHAN 120
DB 61 DPOGWCCTTDBPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLEQAWDSOPHAN 120
QY 121 GYIPSKFPMKNLKNKYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCIX 180
DB 121 GYIPSKFPMKNLKNKYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCIX 180
QY 181 GTGENYRGNAVAVTSQHTCOHWSAQTPHTHERTPENPCKNIDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSQHTCOHWSAQTPHTHERTPENPCKNIDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 241 TNSQVRWEYCKIIPSCDSSPV 260

RESULT 14
AA70255
ID AA70255 standard; protein; 363 AA.
AC AAY70255;
XX
XX 06-JUN-2000 (first entry)
XX
XX Human anglogenesis inhibitor, anglostatin.
XX
XX Human; immunoglobulin gamma Fc fragment; anglostatin; immunofusin;
XX anglogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic;
XX antipsoriatic; antidiabetic; ophthalmological; immunosuppressant;
XX vasectomic; vulnerrary; treatment; antiarteriosclerosis; tumour;
XX metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;
XX ocular anglogenesis disease; diabetic retinopathy; macular degeneration;
XX myocardial anglogenesis; plaque neovascularization; telangiectasia;
XX wound granulation; keloid scar; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200011033-A2.
XX
XX 02-MAR-2000.
XX
XX 25-AUG-1999; 99WO-US019329.
XX
XX 25-AUG-1998; 98US-009783P.
XX
XX (LEXI-) LEXINGEN PHARM CORP.
XX
XX Lo K, Li Y, Gillies SD;
XX
XX WPI; 2000-237616/20.
XX
XX N-PSDB; AA51295.
XX
XX Novel fusion protein of anglostatin or endostatin and an immunoglobulin
XX Fc region, useful for treating conditions mediated by anglogenesis, such
XX as rheumatoid arthritis, tumors and macular degeneration.
XX
XX Example 4; Page 45-46; 68pp; English.
XX
XX The patent discloses a DNA molecule encoding a fusion protein comprising
XX a signal sequence, an immunoglobulin Fc region, and an anglogenesis
XX inhibitor selected from anglostatin, endostatin, a plasmidogen fragment
XX having anglostatin activity, a collagen XVIII fragment having endostatin
XX activity, or combinations of them. The fusion protein (immunofusin) is
XX used to inhibit anglogenesis and to treat diseases or conditions mediated
XX by anglogenesis. Conditions that may be treated include solid tumours,
XX blood born tumours, tumour metastasis, benign tumours including
XX haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic
XX granulomas, rheumatoid arthritis, psoriasis, ocular anglogenetic diseases
XX e.g. diabetic retinopathy, retinopathy of prematurity, macular

```

```

CC degeneration, corneal graft rejection, neovascular glaucoma, retrolental
CC fibroplasia, rubecosis and Oeler-Webber syndrome; myocardial anglogenesis,
CC plaque neovascularisation, telangiectasia, haemophilic joints'
CC angiofibroma, wound granulation, and excessive or abnormal stimulation of
CC endothelial cells, intestinal cells, atherosclerosis, scleroderma and
CC hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in
CC gene therapy. The present sequence is a human anglostatin used in the
CC construction of immunofusin containing human immunoglobulin gamma (1g)
CC Fc fragment
XX
XX Sequence 363 AA;
XX
XX Query Match 99.7%; Score 1535; DB 3; Length 363;
XX Best Local Similarity 99.6%; Pred. No. 2.9e-90;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 VYLSECKTNGKNYGTMSKTNGITCOQWMSSTSPHRRPSPATHPSEGLSENYCRNPDN 60
XX 2 VYLSECKTNGKNYGTMSKTNGITCOQWMSSTSPHRRPSPATHPSEGLSENYCRNPDN 61
DB
QY 61 DPOGWCCTTDBPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLEQAWDSOPHAN 120
DB 62 DPOGWCCTTDBPKRYDYCDILECEBECMHGSGENYDGIKSTMSGLEQAWDSOPHAN 121
QY 121 GYIPSKFPMKNLKNKYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCIX 180
DB 122 GYIPSKFPMKNLKNKYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCIX 181
QY 181 GTGENYRGNAVAVTSQHTCOHWSAQTPHTHERTPENPCKNIDENYCRNPDGKRAPWCHT 240
DB 182 GTGENYRGNAVAVTSQHTCOHWSAQTPHTHERTPENPCKNIDENYCRNPDGKRAPWCHT 241
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 242 TNSQVRWEYCKIIPSCDSSPV 261

RESULT 15
AA702106
ID AA702106 standard; protein; 364 AA.
XX
XX AAY02106;
XX
XX 16-JUL-1999 (first entry)
XX
XX A multifunctional protein of the invention.
XX
XX Anglostatin; endostatin; interferon; thrombospondin;
XX interferon-inducible protein; platelet factor 4; anti-anglogenetic;
XX anti-tumor; multifunctional protein; anglogenetic-mediated disease; cancer;
XX diabetic retinopathy; macular degeneration; arthritis;
XX tumor cell production.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9916889-A1.
XX
XX 08-APR-1999.
XX
XX 30-SEP-1998; 98WO-US020464.
XX
XX 01-OCT-1997; 97US-0060609P.
XX
XX (SEAR ) SEARLE & CO G D.
XX
XX Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;
XX McKearn JP;
XX
XX WPI; 1999-255098/21.
XX
XX New multifunctional proteins useful for treating anglogenetic-mediated
XX diseases.

```

XX Claim 5; Page 101-102; 121pp; English.

CC The specification describes multifunctional proteins which comprise
CC combinations of angiotensin, endostatin, interferon, thrombospondin,
CC interferon-inducible protein and platelet factor 4, and have anti-
CC angiogenic and/or anti-tumor activity. The multifunctional protein may
CC exhibit useful properties such as having similar or greater biological
CC activity when compared to a single factor or by having improved half-life
CC or decreased adverse side effects, or a combination of these properties.
CC The proteins can be used for treating an angiogenic-mediated disease,
CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
CC They can also be used for inhibiting the production of tumor cells
CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
CC in a patient and for inhibiting tumor growth. The present sequence
CC represents a multifunctional protein of the invention

XX
SQ Sequence 364 AA;

Query Match 99.7%; Score 1535; DB 2; Length 364;

Best Local Similarity 99.6%; Pred. No. 2.9e-90; Mismatches 1; Indels 0; Gaps 0;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGKNGKNGTGMSTKTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 60
DB 3 VYLSECKTGKNGKNGTGMSTKTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 62
QY 61 DPOGPMCYTTDPKRYDYCDILFCEBECMHGSGENTDGKISKTMSGLECOAMDOSPHAH 120
DB 63 DPOGPMCYTTDPKRYDYCDILFCEBECMHGSGENTDGKISKTMSGLECOAMDOSPHAH 122
QY 121 GYIPSKFPMKNLKGQNCRNPDRELPRMCFITTDPNKRMELCDIPRCTPPSSSGPTYQCLK 180
DB 123 GYIPSKFPMKNLKGQNCRNPDRELPRMCFITTDPNKRMELCDIPRCTPPSSSGPTYQCLK 182
QY 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPHTERTPENPCNLDENYCRNPDGRAPWCHT 240
DB 183 GTGENYRGNAVAVTVSGHTCOHMSAQTPHTERTPENPCNLDENYCRNPDGRAPWCHT 242
QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 243 TNSQVMEYCKIPSCDSSPV 262

Search completed: January 25, 2006, 17:07:13
Job time : 138 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:02:00 ; Search time 39 Seconds
(without alignments)
641.445 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGNKNGYRGTMK.....TNSQVRWEYCKIPLCDDSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	1335	99.7	810	1 PLNU	plasmin (EC 3.4.21
2	1442	93.6	810	2 B30848	plasmin (EC 3.4.21
3	1292	83.9	790	1 PLPG	plasmin (EC 3.4.21
4	1291	83.8	812	1 PLBO	plasmin (EC 3.4.21
5	1274	82.7	812	1 PLMS	plasmin (EC 3.4.21
6	1237	80.3	810	2 T18518	plasmin (EC 3.4.21
7	881	57.2	2869	2 T18518	apolipoprotein(a)
8	797	51.8	728	1 JH0579	hepatocyte growth
9	782	50.4	728	1 A35644	hepatocyte growth
10	776.5	50.4	710	1 T51283	hepatocyte growth
11	766.5	49.8	728	1 A60185	hepatocyte growth
12	754.5	49.0	716	1 JCS061	macrophage-stimula
13	753.5	48.9	716	1 A40332	macrophage-stimula
14	749	48.6	4548	1 S00657	apoptocytin(a) (EC
15	739	48.0	711	1 A47136	macrophage-stimula
16	739	48.0	1420	2 A32869	apolipoprotein(a)
17	739	48.0	1420	2 A32869	apolipoprotein(a)
18	505	32.8	455	2 A61545	plasmin (EC 3.4.21
19	499	32.4	460	2 B61545	plasmin (EC 3.4.21
20	391.5	25.4	336	2 S33879	plasmin precursor
21	372	24.2	625	2 T8BO	chrombin (EC 3.4.2
22	362.5	23.5	169	2 A40522	chrombin (EC 3.4.2
23	357.5	23.2	618	2 A35827	chrombin (EC 3.4.2
24	351	22.8	622	1 T8BU	chrombin (EC 3.4.2
25	348	22.6	617	2 S10511	chrombin (EC 3.4.2
26	309.5	19.1	562	1 UKHUT	t-plasminogen acti
27	295.5	19.2	559	1 A35029	t-plasminogen acti
28	281.5	18.3	559	1 A29941	t-plasminogen acti
29	278	18.1	120	2 B61545	plasmin (EC 3.4.21

30	271	17.6	89	2 A60140	plasmin (EC 3.4.21
31	268	17.4	123	2 C61545	plasmin (EC 3.4.21
32	241.5	15.7	937	2 A45082	neurotrophic recep
33	240	15.6	943	2 B45082	neurotrophic recep
34	237.5	15.4	946	1 A47299	for-related recep
35	233	15.1	603	2 S28941	coagulation factor
36	214	13.9	558	2 JCS878	plasma hyaluronan-
37	210	13.6	560	1 JCS4795	plasma hyaluronan-
38	201	13.1	291	2 T18098	t-plasminogen acti
39	198	12.9	615	1 KFHU12	coagulation factor
40	190.5	12.4	593	2 S45281	coagulation factor
41	188.5	12.2	655	2 A46688	hepatocyte growth
42	178.5	11.6	806	2 T18840	hypothetical prote
43	165	10.7	433	1 UN0560	u-plasminogen acti
44	153	9.9	442	1 UKRG	u-plasminogen acti
45	151	9.8	432	1 S18932	u-plasminogen acti

ALIGNMENTS

RESULT 1

PLNU
plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [monomer]
N:Contains: angiotensin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A0
R:Peterson, T.E.; Martzen, M.R.; Ichihara, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A>Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr
A:Reference number: A35229; MUID:90202879; PMID:2318848
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1-810 <PEP>
A:Cross-references: UNIPARC:P00747; UNIPROT:Q9UB09; UNIPROT:Q9UM12; UNIPARC:UPI000016ABK
A:Experimental source: leukocyte, lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; T
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A>Title: Definition of the transcription initiation site of human plasminogen gene in 1
A:Reference number: I52242; MUID:91097523; PMID:2268308
A:Accession: I52242
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL>
A:Cross-references: UNIPARC:UPI0000062A8; GB:M62890; NID:G190092; PIDN:AAA36454.1; PID
R:Forstgen, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A>Title: Molecular cloning and characterization of a full-length cDNA clone for human p
A:Reference number: A26646; MUID:87162490; PMID:3030813
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: UNIPARC:UPI000000DB8; GB:X05199; NID:G35530; PIDN:CAA28831.1; PID:
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A>Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A:Reference number: I45961; MUID:85023311; PMID:6148861
A:Accession: I45961
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: UNIPARC:UPI000016ABD4; GB:X02922; NID:G190112; PIDN:AAA60124.1; PID:
A:Accession: I84609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: UNIPARC:UPI0000071C7D; GB:X02921; NID:G190110; PIDN:AAA60123.1; PID:
R:Brundish, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,

C/Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F.1-96/Domains: plasminogen-related protein precursor homology <PLPH>
 F.1-19/Domains: signal sequence #status predicted <SIG>
 F.20-810/Product: plasminogen #status experimental <PRO>
 F.20-810/Product: activation peptide #status experimental <APt>
 F.79-86/Product: angiotensin #status experimental <AST>
 F.97-580,581-810/Product: plasmin #status experimental <MAT>
 F.97-580/Domains: plasmin chain A #status experimental <CHA>
 F.103-181/Domains: kringle homology <KR1>

Query Match 99.7%; Score 1535; DB 1; Length 810;
 Best Local Similarity 99.6%; Pred. No. 1.6e-104;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 VLSSEKTKNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCNPN 60
 98 VLSSEKTKNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCNPN 157
 61 DPGPWCYTTPDEPRKDYCDILECEBCHGSGENYDGIKSTMSGLEQAMDSQSPH 120
 158 DPGPWCYTTPDEPRKDYCDILECEBCHGSGENYDGIKSTMSGLEQAMDSQSPH 217
 121 GIIPSKFPKKNLKNYCRNPDLRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQC 180
 218 GIIPSKFPKKNLKNYCRNPDLRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQC 277
 181 GGENYRGVAATVSGHTQHSACQPHTHETPENFPCKNDENYCRNPDGRAPWCH 240
 278 GGENYRGVAATVSGHTQHSACQPHTHETPENFPCKNDENYCRNPDGRAPWCH 337
 241 TNSQVRWEYCKIPSCDSSPV 260
 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2

B30848
 Plasmin (BC 3.4.21.7) precursor - rhesus macaque
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 31-Mar-1989 #sequence__revision 31-Mar-1989 #text_change 09-Jul-2004
 C/Accession: B32869; B30848
 R/Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A/Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A/Reference number: A32869; MUID:89174660; PMID:2525643
 A/Accession: B32869
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-810 <TOM>
 A/Cross-references: UNIPROT:P12545; UNIPARC:UPI0000131COP; GB:J04697; NID:9342272; PIND:
 C/Superfamily: Plasmin; kringle homology; plasminogen-related protein precursor homology
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F.1-96/Domains: plasminogen-related protein precursor homology <PLPH>
 F.1-9/Domains: signal sequence #status predicted <SIG>
 F.103-181/Domains: kringle homology <KR1>
 F.185-262/Domains: kringle homology <KR2>
 F.275-352/Domains: kringle homology <KR3>
 F.377-454/Domains: kringle homology <KR4>
 F.481-560/Domains: kringle homology <KR5>
 F.581-803/Domains: trypsin homology <TRY>
 F.49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F.622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2; Length 810;
 Best Local Similarity 93.1%; Pred. No. 9.4e-98;
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

1 VLSSEKTKNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCNPN 60
 98 VLSSEKTKNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLEENYCNPN 157
 61 DPGPWCYTTPDEPRKDYCDILECEBCHGSGENYDGIKSTMSGLEQAMDSQSPH 120

156 DPGPWCYTTPDEPRDYCDILECEBCHGSGENYDGIKSTMSGLEQAMDSQSPH 217
 121 GIIPSKFPKKNLKNYCRNPDLRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQC 180
 218 GIIPSKFPKKNLKNYCRNPDLRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQC 277
 181 GGENYRGVAATVSGHTQHSACQPHTHETPENFPCKNDENYCRNPDGRAPWCH 240
 278 GGENYRGVAATVSGHTQHSACQPHTHETPENFPCKNDENYCRNPDGRAPWCH 337
 241 TNSQVRWEYCKIPSCDSSPV 260
 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3

PLPG
 plasmin (BC 3.4.21.7) precursor - pig (fragment)
 N/Alternate names: plasminogen
 N/Contains: miniplasminogen
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 07-Sep-1990 #sequence__revision 01-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S03733; S03737; A25834
 R/Schaller, J.; Marti, T.; Roesele, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A/Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the c
 A/Reference number: S03733
 A/Accession: S03733
 A/Molecule type: protein
 A/Residues: 1-560 <SCH>
 A/Cross-references: UNIPROT:P06867; UNIPARC:UPI0000172B90
 R/Brunisholz, R.A.; Letch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.,
 Eur. J. Biochem. 114, 465-470, 1981
 A/Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
 A/Reference number: S03735; MUID:81212097; PMID:7238497
 A/Accession: S03737
 A/Molecule type: protein
 A/Residues: 1-57 <BRU>
 A/Cross-references: UNIPARC:UPI0000172B91
 R/Marti, T.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A/Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
 A/Reference number: A25834; MUID:85203907; PMID:3846533
 A/Accession: A25834
 A/Molecule type: protein
 A/Residues: 450-790 <MAR>
 A/Cross-references: UNIPARC:UPI0000172B92
 C/Function:
 A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ne the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A/pathway: fibrinolysis
 C/Superfamily: Plasmin; kringle homology; plasminogen-related protein precursor homology
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
 F.1-790/Product: plasminogen #status predicted <PRO>
 F.1-77/Domains: plasminogen-related protein precursor homology (fragment) <PLPH>
 F.78-560/Product: activation peptide #status predicted <APt>
 F.84-162/Domains: kringle homology <KR1>
 F.166-243/Domains: kringle homology <KR2>
 F.256-333/Domains: kringle homology <KR3>
 F.358-435/Domains: kringle homology <KR4>
 F.450-790/Product: miniplasminogen #status experimental <MIN>
 F.461-540/Domains: kringle homology <KR5>
 F.561-790/Product: plasmin chain B #status experimental <BGH>
 F.561-783/Domains: trypsin homology <TRY>
 F.30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
 bonds: #status predicted
 F.602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1; Length 790;
 Best Local Similarity 81.4%; Pred. No. 8e-87;
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

eful in treating solid tumors.

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domain: activation peptide #status predicted <APT>

F:79-466/Product: angiotensin #status predicted <AST>

F:97-581-812/Product: plasmin #status predicted <MAT>

F:97-581/Domain: chain A #status predicted <ACH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:275-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:582-812/Domain: chain B #status predicted <BGH>

F:582-805/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32

Bonds: #status predicted

F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136,308/Binding site: carboxylate (Asn) (covalent) #status predicted

F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 82.7%; Score 1274; DB 1; Length 812;

Best Local Similarity 80.6%; Pred. No. 1.7e-85;

Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNGYRGMTSKNGITGQKWSSTSPRRPSPATHPSEGLSENYCNPND 60

DB 98 VLSCKTGNGKNGYRGMTSKNGITGQKWSSTSPRRPSPATHPSEGLSENYCNPND 157

QY 61 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLGEOANDSOPH 120

DB 158 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLGEOANDSOPH 217

QY 121 GYPSKFPKNNKKYCRNPDBELRPWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 180

DB 218 GYPSKFPKNNKKYCRNPDBELRPWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 277

QY 181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLDENYCRNPDGRAPWCH 240

DB 278 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLDENYCRNPDGRAPWCH 337

QY 241 TNSQVMEYCKIPSCDSS 258

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:379-456/Domain: kringle homology <KR4>
F:482-561/Domain: kringle homology <KR5>
F:582-803/Domain: trypsin homology <TRY>

Query Match 80.3%; Score 1237; DB 2; Length 810;

Best Local Similarity 79.9%; Pred. No. 8.4e-83;

Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNGYRGMTSKNGITGQKWSSTSPRRPSPATHPSEGLSENYCNPND 60

DB 98 VLSCKTGNGKNGYRGMTSKNGITGQKWSSTSPRRPSPATHPSEGLSENYCNPND 157

QY 61 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLGEOANDSOPH 120

DB 158 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLGEOANDSOPH 217

QY 121 GYPSKFPKNNKKYCRNPDBELRPWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 180

DB 218 GYPSKFPKNNKKYCRNPDBELRPWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 277

QY 181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLDENYCRNPDGRAPWCH 240

DB 278 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLDENYCRNPDGRAPWCH 337

QY 241 TNSQVMEYCKIPSCDSS 258

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

F:185-262/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR3>
F:379-456/Domain: kringle homology <KR4>
F:482-561/Domain: kringle homology <KR5>
F:582-803/Domain: trypsin homology <TRY>

Query Match 80.3%; Score 1237; DB 2; Length 810;

Best Local Similarity 79.9%; Pred. No. 8.4e-83;

Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNGYRGMTSKNGITGQKWSSTSPRRPSPATHPSEGLSENYCNPND 60

DB 98 VLSCKTGNGKNGYRGMTSKNGITGQKWSSTSPRRPSPATHPSEGLSENYCNPND 157

QY 61 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLGEOANDSOPH 120

DB 158 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLGEOANDSOPH 217

QY 121 GYPSKFPKNNKKYCRNPDBELRPWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 180

DB 218 GYPSKFPKNNKKYCRNPDBELRPWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 277

QY 181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLDENYCRNPDGRAPWCH 240

DB 278 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLDENYCRNPDGRAPWCH 337

QY 241 TNSQVMEYCKIPSCDSS 258

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

QY 338 TNSQVMEYCKIPSCDSS 355

DB 338 TNSQVMEYCKIPSCDSS 355

RESULT 8
 hepatocyte growth factor precursor [validated] - human
 JH0579
 N/Alternate names: heparinectin A; scatter factor
 C/Species: Homo sapiens (man)
 C/Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text change 09-Jul-2004
 C/Accession: JH0579; J00333; A41140; B36677; A33512; A39006; PH0114; A3796; S06
 R/Seki, T.; Hagiya, M.; Shimoniishi, M.; Nakamura, T.; Shimizu, S.
 Gene 102, 213-219, 1991
 A/Title: Organization of the human hepatocyte growth factor-encoding gene.
 A/Reference number: JH0579; MUID:91340155; PMID:1831432
 A/Accession: JH0579
 A/Molecule type: DNA
 A/Residues: 1-728 <SE>
 A/Cross-references: UNIPROT:P14210, UNIPARC:UPI000000D92B, DDBJ:D90318
 A/Note: the authors translated the codon GAA for residue 662 as Gly
 R/Seki, T.; Hagiya, M.; Shimoniishi, M.; Nakamura, T.; Shimizu, S.
 submitted to JPID, March 1991
 A/Description: Organization of the human hepatocyte growth factor-encoding gene.
 A/Reference number: J00333
 A/Accession: J00333
 A/Molecule type: DNA
 A/Residues: 1-481, 'RT', 484-728 <SE2>
 A/Cross-references: UNIPARC:UPI0000172B97
 R/Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
 Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
 A/Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor
 A/Reference number: A41140; MUID:91343493; PMID:1831266
 A/Accession: A41140
 A/Molecule type: mRNA
 A/Residues: 1-728 <SE1>
 A/Cross-references: UNIPARC:UPI000000D92B, GB:M72339, NID:9337935, PIDN:AAA64239.1; PID:
 R/Seki, T.; Ihara, I.; Sugimura, A.; Shimoniishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
 Biochem. Biophys. Res. Commun. 172, 321-327, 1990
 A/Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor
 A/Reference number: A36677; MUID:91025062; PMID:2145636
 A/Accession: B36677
 A/Molecule type: mRNA
 A/Residues: 1-728 <SE3>
 A/Cross-references: UNIPARC:UPI000000D92B; GB:M60718; NID:9184031; PIDN:AAA52648.1; PID:
 A/Accession: A36677
 A/Molecule type: mRNA
 A/Residues: 1-161, 167-728 <SE4>
 A/Cross-references: UNIPARC:UPI0000146316; EMBL:X16323
 A/Experimental source: leukocyte
 R/Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
 Biochem. Biophys. Res. Commun. 163, 967-973, 1989
 A/Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
 A/Reference number: A33512; MUID:89392017; PMID:2528952
 A/Accession: A33512
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-728 <MY>
 A/Cross-references: UNIPARC:UPI000000D92B; GB:M29145; NID:9184041; PIDN:AAA52650.1; PID:
 R/Rubin, U.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hix
 Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
 A/Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte
 A/Reference number: A39006; MUID:91110540; PMID:1824873
 A/Accession: A39006
 A/Molecule type: mRNA
 A/Residues: 1-161, 167-728 <RUB>
 A/Cross-references: UNIPARC:UPI0000146316; GB:M55379
 A/Experimental source: embryonic lung
 R/Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
 Biochem. Biophys. Res. Commun. 175, 660-667, 1991
 A/Title: Identification of the N-terminal residue of the heavy chain of both native and
 A/Reference number: PH0114, MUID:91207365; PMID:1826837
 A/Accession: PH0114
 A/Molecule type: protein
 A/Residues: 32-43; 53-58 <YOS>
 A/Cross-references: UNIPARC:UPI0000172B98; UNIPARC:UPI0000172B99

A/Experimental source: plasma
 R/Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
 J. Cell Biol. 111, 2097-2108, 1990
 A/Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
 A/Reference number: A37796; MUID:91035621; PMID:2146276
 A/Accession: A37796
 A/Molecule type: protein
 A/Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X', 5
 A/Cross-references: UNIPARC:UPI0000172B9A; UNIPARC:UPI0000172B9B; UNIPARC:UPI0000172B9C;
 R/Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimoniishi, M.; Sugimura, A.; Teshi
 Nature 342, 440-443, 1989
 A/Title: Molecular cloning and expression of human hepatocyte growth factor.
 A/Reference number: S06794; MUID:9006676; PMID:2531289
 A/Accession: S06794
 A/Molecule type: mRNA
 A/Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'M', 301-316, 'A', 318-335, 'K', 337-386, '
 A/Cross-references: UNIPARC:UPI000015624E; EMBL:X16323; NID:932081; PIDN:CAA34387.1; PID:
 A/Experimental source: liver
 A/Note: the authors translated the codon CAG for residue 727 as Glu
 R/Hartmann, G.; Maldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
 Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
 A/Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
 A/Reference number: 159214; MUID:93087571; PMID:1280830
 A/Accession: 159214
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-288, 'ET', 'HAR>
 A/Cross-references: UNIPARC:UPI0000073BF9; GB:J02931; NID:9184033; PIDN:AAA52649.1; PID:
 R/Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
 Eur. J. Biochem. 197, 15-22, 1991
 A/Title: An alternatively processed mRNA generated from human hepatocyte growth factor g
 A/Reference number: S15443; MUID:91200041; PMID:182653
 A/Accession: S15443
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-288, 'ET' <MY2>
 A/Cross-references: UNIPARC:UPI0000073BF9; EMBL:X57574; NID:932083; PIDN:CAA40802.1; PID:
 R/Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
 A/Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
 A/Reference number: 152253; MUID:92062058; PMID:1833383
 A/Accession: 152253
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 161-166 <SHI>
 A/Cross-references: UNIPARC:UPI00000353AB; GB:S62561; NID:9237996; PIDN:AA820169.1; PID:
 C/Genetics:
 A/Gene: GDB:HG
 A/Cross-references: GDB:127524; OMIM:142409
 A/Map position: 7q21.1-7q21.1
 A/Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48
 C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C/Function:
 A/Description: stimulates mitosis of hepatocytes and other cells
 A/Note: does not have proteinase activity
 C/Superfamily: hepatocyte growth factor/microphage stimulating protein 1; kringle homolc
 C/Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
 F/1-31/Domain: signal sequence #status predicted <SIG>
 F/32-494/Domain: Product: hepatocyte growth factor #status experimental <MAT>
 F/32-494/Domain: alpha chain #status experimental <ACH>
 F/128-206/Domain: kringle homology <KR1>
 F/211-288/Domain: kringle homology <KR2>
 F/305-383/Domain: kringle homology <KR3>
 F/391-469/Domain: kringle homology <KR4>
 F/495-728/Domain: beta chain #status experimental <BCH>
 F/395-716/Domain: tryptophan homology <TR>
 F/32/modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
 F/294, 402, 566, 653/binding site: carbohydrate (Asn) (covalent) #status predicted
 F/487-604/disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;
 Best Local Similarity 51.0%; Pred. No. 9; 4e-51;

Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;

OY 2 YLSBCKTNGKNRYGCTMSKTNIGTCQKWSSTSPRRPSPATPHBSGLENYCRNPND 61
Db 124 YLRNCLTGKRSYKGTAVITSKGICQPWSSMIPIHESFLPSYSRGKLQENYCRNPGE 183
OY 62 PQGPCYTDEKRVDCVDILIECE-ECMHSGSENYDOKISKTMISGLECQAMDSQSPAH 120
Db 184 EGGPCFSPNEBRVEVCDIPQCSVEECMTNGSRYELMHTSGIKIQRMWDQTPIRH 243
OY 121 GYIESPFNKULKKYVCANPDRELPMCFITDPNKRWECDIIPCRC--TTPESSGP--TY 176
Db 244 KFLPERYDKDFDDNYCNPDOGRPKCYTDLPHTRMYCAIKTCADTMDTDVPLETT 303
OY 177 QCLKGTGENYRGNVAVTVSQHTCOHSAQOTPHERTETEPNCPXNLDENYCRNPDGRAP 236
Db 304 ECIOOGEGYGTVWTINWGIPCORWSDSQYDHEHDMTPEFKDXDLRENTCRNPDGSBP 363
OY 237 WCHTNSQVRWEYC-KIPSCDS 258
Db 364 WCFTDPNIRVGYSQIPNCDS 386

RESULT 9

A35644
hepatocyte growth factor precursor - rat
N:Alternate names: hepatietin A; scatter factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
C:Accession: A35644; S13211
R:Tashiro, K.; Hagiyama, T.; Nishizawa, T.; Seki, T.; Shimomishi, M.; Shimizu, S.; Nakamura,
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A>Title: Deduced primary structure of rat hepatocyte growth factor and expression of the
A:Reference number: A35644; MUID:90222197; PMID:2139229
A:Accession: A35644
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-728 <TAS>
A:Cross-references: UNIPROT:P17945; UNIPARC:UPI000012C6D3; GB:D90102; GI:IM32987; NID:G222
A>Note: The authors translated the codon GAG for residue 70 as Gin, GAC for residue 417
R:Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A>Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur
A:Reference number: S13211; MUID:91031482; PMID:2146117
A:Accession: S13211
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-728 <OKA>
A:Cross-references: UNIPARC:UPI000012C6D3; EMBL:X54400; NID:G56353; PIDN:CAA38266.1; PII
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Function:
A:Description: stimulates mitosis of hepatocytes and other cells
C:Superfamily: hepatocyte growth factor/microphage stimulating protein 1; kringle homology
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyruvate
F:1-32/Domain: signal sequence #status predicted <SIG>
F:56-495/Product: hepatocyte growth factor #status predicted <MAT>
F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:129-207/Domain: kringle homology <KR1>
F:212-289/Domain: kringle homology <KR2>
F:306-384/Domain: kringle homology <KR3>
F:392-470/Domain: kringle homology <KR4>
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BGH>
F:496-719/Domain: trypsin homology <TRY>
F:333/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicee
F:293,403,569,556/Binding site: carbonhydrate (Asn) (covalent) #status predicted
F:488-607/Disulfide bonds: #status predicted

Query Match 50.8%; Score 782; DB 1; Length 728;
Best Local Similarity 49.8%; Pred. No. 1,2e+49;
Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;

2 YLSBCKTNGKNRYGCTMSKTNIGTCQKWSSTSPRRPSPATPHBSGLENYCRNPND 61

Db

125 YIRNCITIGKGSYKGTVAITTKSGIKCPWNMSI.PHEHSFLPSSRKGDLQENYCNPGE 184
62 POGPWCYTTDPKKRYDYCDILECEE--ECMHSGSENYDGKISKTMSGLECOAMDQSPPAH 120
185 EGGPWCFTPSNPEVRREVCDIPCCSEVEMCTCNESYRGPMDDHTSNGKTCQAMDOQTPIRH 244
Oy 121 GYIPSKFPNNKLKNKYCRNPDRELPRWCFCTTDPNKAMELCDIPRCT-----TPPSSGP 174
245 KFLPERVPDCKGFDNDYCRNPDCKFRPWCYTLLDPTDPEYCAIKCASHAVNETIVPME-- 302
Db 175 TYOCLKGGSENRGNVAATVSCHTQHWASQFTHERTETPENPKULDENYCRNPDCKR 234
303 TTCECKGGGBGRGTTNTIWTNGIPCCRMDSQYPHKDITDENPKCKDLRENYCRNPDAE 362
Oy 235 APWCATTNSQVAREYC-KIPSCDSS 258
363 SPWCFTTDPNIRVGYSQIPIKCDVS 387
Db

RESULT 10
151283
hepatocyte growth factor precursor - clawed frog
N.Alternate names: hepatoinetin A; scatter factor
C.Species: Xenopus sp. (clawed frog)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-May-2004
C.Accession: I51283
R.Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
Mech. Dev. 49, 123-131, 1995
A.Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear
A.Reference number: I51283; MUID:95267650; PMID:7748783
A.Accession: I51283
A>Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-710 <NA>
A.Cross-references: UNIPARC:UPI00000PDER6; GB:S77422; NID:g9989932; PIDN:AABJ4354.1; PID
A.Note: The authors' translation for residue 458 (Thr) is inconsistent with the nucleoti
C.Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C.Function:
A.Description: stimulates mitosis of hepatocytes and other cells
A>Note: does not have proteinase activity
C.Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C.Keywords: duplication; glycoprotein; growth factor; heterodimer; Kringle
F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <MAT>
F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:115-193/Domain: kringle homology <KR1>
F:198-275/Domain: kringle homology <KR2>
F:289-367/Domain: kringle homology <KR3>
F:375-453/Domain: kringle homology <KR4>
F:478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F:478-709/Domain: trypsin homology <TRY>
F:552,128,281,332,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre
F:470-588/Dnaulflde bonds: #status predicted

Query Match 50.4%; Score 776.5; DB 1; Length 710;
Best Local Similarity 50.0%; Pred. No.2,9e-49;
Matches 130; Conservative 39; Mismatches 88; Indels 3; Gaps 3;

Oy 2 YLSBEKTNKGNKRYRTSMKTRKNGITCOKWSSTSPHPRPREPATHPBSGLBNYCRNPND 61
111 YIRDCITHKGSYRGRTRNTYKRGALACPWNMSI.PHEHSFLPSSRKGDLKENYCNPGE 170
Db

Oy 62 POGPWCYTTDPKKRYDYCDILECEE--ECMHSGSENYDGKISKTMSGLECOAMDQSPPAH 120
171 EGGPWCFTPSNPEVRREVCDIPCCSEVEMCTCNESYRGPMDDHTSNGKTCQAMDOQTPIRH 230
Db

Oy 121 GYIPSKFPNNKLKNKYCRNPDRELPRWCFCTTDPNKAMELCDIPRCT.-TPPSSGP 179
231 KFLPERVPDCKGFDNDYCRNPDCKFRPWCYTLLDPTDPEYCAIKCASHAVNETIVPME-- 290
Db

Oy 180 KGTEGNRYGNVAATVSCHTQHWASQFTHERTETPENPKULDENYCRNPDCKRAAPCH 239
291 KGQGEGYGVASTTYTNGIQCCQMDSQPHLHNTPPENYKCKDISENYCRNPDGSESSEPCP 350
Db

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Comphen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:11:02 ; Search time 32 Seconds
(without alignments)
87.986 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540
Sequence: 1 VLSSECKTNGKNGKNGTMSK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10823074 residues
Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1535	99.7	339	7	US-11-010-874-3 Sequence 3, App1
2	1535	99.7	567	6	US-10-995-561-764 Sequence 764, App
3	1535	99.7	791	7	US-11-056-621-4 Sequence 4, App1
4	1535	99.7	810	6	US-10-995-561-761 Sequence 761, App
5	1535	99.7	810	6	US-10-995-561-761 Sequence 2, App1
6	1442	93.6	339	7	US-11-010-874-4 Sequence 4, App1
7	1292	84.2	339	7	US-11-010-874-6 Sequence 6, App1
8	1292	84.2	339	7	US-11-010-874-5 Sequence 5, App1
9	1274	82.7	339	7	US-11-010-874-2 Sequence 2, App1
10	1274	82.7	812	7	US-11-010-874-1 Sequence 1, App1
11	1001	65.0	168	7	US-11-010-874-8 Sequence 8, App1
12	954	61.9	168	7	US-11-010-874-9 Sequence 9, App1
13	952	61.8	160	7	US-11-010-874-13 Sequence 13, App1
14	896	58.2	160	7	US-11-010-874-14 Sequence 14, App1
15	883	57.3	168	7	US-11-010-874-10 Sequence 10, App1
16	881	57.2	168	7	US-11-010-874-11 Sequence 11, App1
17	847	55.0	168	7	US-11-010-874-7 Sequence 7, App1
18	801	52.0	160	7	US-11-010-874-16 Sequence 16, App1
19	799	51.9	160	7	US-11-010-874-15 Sequence 15, App1
20	797	51.8	160	7	US-11-010-874-12 Sequence 12, App1
21	797	51.8	728	7	US-11-124-635-6 Sequence 6, App1
22	797	51.8	728	7	US-11-124-635-8 Sequence 8, App1
23	797	51.8	728	7	US-11-043-788-164 Sequence 164, App
24	749	48.6	1169	6	US-10-995-561-609 Sequence 609, App
25	749	48.6	1169	7	US-11-124-368-228 Sequence 228, App

26	711	46.2	308	7	US-11-162-817-11 Sequence 11, App1
27	643	41.8	648	7	US-11-127-877-72 Sequence 72, App1
28	531.5	34.5	290	7	US-11-043-788-165 Sequence 165, App
29	524.5	34.1	296	7	US-11-043-788-168 Sequence 168, App
30	320	20.8	516	6	US-10-995-561-559 Sequence 559, App
31	309.5	20.1	527	6	US-10-705-633-1 Sequence 1, App1
32	309.5	20.1	527	6	US-10-705-633-2 Sequence 2, App1
33	309.5	20.1	527	6	US-10-705-633-3 Sequence 3, App1
34	309.5	20.1	562	6	US-10-995-561-561 Sequence 561, App
35	293	19.0	482	6	US-10-995-561-560 Sequence 560, App
36	270.5	17.6	79	7	US-11-010-874-17 Sequence 17, App1
37	258.5	16.8	86	7	US-11-162-817-2 Sequence 2, App1
38	246.5	16.0	205	7	US-11-043-788-166 Sequence 166, App
39	219	14.2	61	6	US-10-995-561-762 Sequence 762, App
40	219	14.2	136	6	US-10-995-561-760 Sequence 760, App
41	205	13.3	293	6	US-10-995-561-562 Sequence 562, App
42	204	13.2	291	6	US-10-995-561-558 Sequence 558, App
43	198	12.9	641	7	US-11-094-519A-29 Sequence 29, App1
44	168	10.9	473	6	US-10-509-464-5 Sequence 5, App1
45	164.5	10.7	473	6	US-10-509-464-6 Sequence 6, App1

ALIGNMENTS

```

RESULT 1
US-11-010-874-3
; Sequence 3, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FILE REFERENCE: 5820.656
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-010-874-3
Query Match          99.7%; Score 1535; DB 7; Length 339;
Best Local Similarity 99.6%; Pred. No. 6.2e-119;
Matches 259; Conserved 0; Mismatches 1; Indels 0; Gaps 0;
1 VLSSECKTNGKNGKNGTMSKNGITCKWSTSPRRPSPATPSBGLBENYCRNPN 60
1 VLSSECKTNGKNGKNGTMSKNGITCKWSTSPRRPSPATPSBGLBENYCRNPN 60
61 DPGWCCTTPEKRYDCDILECEBCHGSGENYDKISKTMSGLBQANDSOPHAN 120
61 DPGWCCTTPEKRYDCDILECEBCHGSGENYDKISKTMSGLBQANDSOPHAN 120
121 GYIPKFPKNIKKNYCRNPDELRPWCTTDPNTRKWEICDIPRCTTPSSGPTYQCL 180
121 GYIPKFPKNIKKNYCRNPDELRPWCTTDPNTRKWEICDIPRCTTPSSGPTYQCL 180
121 GYIPKFPKNIKKNYCRNPDELRPWCTTDPNTRKWEICDIPRCTTPSSGPTYQCL 180
121 GYIPKFPKNIKKNYCRNPDELRPWCTTDPNTRKWEICDIPRCTTPSSGPTYQCL 180
181 GTGSEYRGNVATVSGHCOHWSAOTPHTRHTPENPCKNDENYCRNPDGRAPWCHT 240
181 GTGSEYRGNVATVSGHCOHWSAOTPHTRHTPENPCKNDENYCRNPDGRAPWCHT 240
241 TNSQVRWEYCKIPSCDSSPV 260
241 TNSQVRWEYCKIPSCDSSPV 260
241 TNSQVRWEYCKIPSCDSSPV 260

```

```
RESULT 2
US-10-995-561-764
; Sequence 764, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 764
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-764

Query Match          99.7%; Score 1535; DB 6; Length 567;
Best Local Similarity 99.6%; Pred. No. 1e-118;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSSGLEENYCRNPND 60
DB 98 VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSSGLEENYCRNPND 157
QY 61 DPGPWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECOANDSOPHAA 120
DB 158 DPGPWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECOANDSOPHAA 217
QY 121 GYIPSKFPKNLKKNYCRNPDELPRMCFCTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
DB 218 GYIPSKFPKNLKKNYCRNPDELPRMCFCTTDPNKMELCDIPRCTTPPSSGPTYQCLK 277
QY 181 GTGENTYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDKRAPWCMT 240
DB 278 GTGENTYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDKRAPWCMT 337
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 338 TNSQVRWEYCKIIPSCDSSPV 357

RESULT 3
US-11-056-621-4
; Sequence 4, Application US/11056621
; Publication No. US20050262592A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; APPLICANT: Dickey, Lynn F.
; APPLICANT: Gadsaka, John R.
; APPLICANT: Wang, Xiaowei
; APPLICANT: Cox, Kevin M.
; APPLICANT: Peele, Charles G.
; TITLE OF INVENTION: EXPRESSION OF PLASMINOGEN AND
; TITLE OF INVENTION: MICROPOLYMERIZATION IN DUCKWEED
; FILE REFERENCE: 40989/274646
; CURRENT APPLICATION NUMBER: US/11/056,621
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,487
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of mature human plasminogen
```

```
US-11-056-621-4

Query Match          99.7%; Score 1535; DB 7; Length 791;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSSGLEENYCRNPND 60
DB 79 VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSSGLEENYCRNPND 138
QY 61 DPGPWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECOANDSOPHAA 120
DB 139 DPGPWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECOANDSOPHAA 198
QY 121 GYIPSKFPKNLKKNYCRNPDELPRMCFCTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
DB 199 GYIPSKFPKNLKKNYCRNPDELPRMCFCTTDPNKMELCDIPRCTTPPSSGPTYQCLK 258
QY 181 GTGENTYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDKRAPWCMT 240
DB 259 GTGENTYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDKRAPWCMT 318
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 319 TNSQVRWEYCKIIPSCDSSPV 338

RESULT 4
US-10-995-561-761
; Sequence 761, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-761

Query Match          99.7%; Score 1535; DB 6; Length 810;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSSGLEENYCRNPND 60
DB 98 VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSSGLEENYCRNPND 157
QY 61 DPGPWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECOANDSOPHAA 120
DB 158 DPGPWCYTTDPKRYDYCDILCEBECMHCSENGYDGIKSTMSGLECOANDSOPHAA 217
QY 121 GYIPSKFPKNLKKNYCRNPDELPRMCFCTTDPNKMELCDIPRCTTPPSSGPTYQCLK 180
DB 218 GYIPSKFPKNLKKNYCRNPDELPRMCFCTTDPNKMELCDIPRCTTPPSSGPTYQCLK 277
QY 181 GTGENTYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDKRAPWCMT 240
DB 278 GTGENTYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDKRAPWCMT 337
QY 241 TNSQVRWEYCKIIPSCDSSPV 260
DB 338 TNSQVRWEYCKIIPSCDSSPV 357

RESULT 5
```

```

US-10-220-824-2
; Sequence 2, Application US/10220824
; Publication No. US20050277603A1
; GENERAL INFORMATION:
; APPLICANT: Viewmed Limited
; TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a
; TITLE OF INVENTION: gene encoding an anti-angiogenic protein or parts thereof
; FILE REFERENCE: OP0208/PCT
; CURRENT APPLICATION NUMBER: US/10/220,824
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: KR 2001-000691
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Kopacentin 1.71
; SEQ ID NO 2
; LENGTH: 810
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-220-824-2

```

Query Match	99.7%	Score 1535;	DB 6;	Length 810;
Best Local Similarity	99.6%	Pred. No. 1.4e-118;		
Matches 259; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	YLVSCKTGNKNGYGTMSKTNGJITCQKMSSTS	PHRPRFSPATHSEGLEENYCNPN	60
Db	98	YLSCKTGNKNGYGTMSKTNGJITCQKMSSTS	PHRPRFSPATHSEGLEENYCNPN	157
Qy	61	DPQGFWCTTTPBEKRYDYCDLIECBECMHSGENYDKI	SKTMSGLECOAMDOSPHAH	120
Db	158	DPOGFWCTTTPBEKRYDYCDLIECBECMHSGENYDKI	SKTMSGLECOAMDOSPHAH	217
Qy	121	GYIPKPFNKJLKKNYCRNPDRRLPWCFTTTPNKKWEI	CDIPRCTTPPSSGPTYOCLK	180
Db	218	GYIPKPFNKJLKKNYCRNPDRRLPWCFTTTPNKKWEI	CDIPRCTTPPSSGPTYOCLK	277
Qy	181	GTGENYRGNVAVTVSAGHTCQHMSAOTPHHRT	PHENFPCKNLDENYCRNPDGRAPWCHT	240
Db	278	GTGENYRGNVAVTVSAGHTCQHMSAOTPHHRT	PHENFPCKNLDENYCRNPDGRAPWCHT	337
Qy	241	TNSQVRWEYCKIPSCDSSPV	260	
Db	338	TNSQVRWEYCKIPSCDSSPV	357	

RESULT 6
US-11-010-874-4

```

? Sequence 4, Application US/11010874
? Publication No. US20050250694A1
? GENERAL INFORMATION:
? APPLICANT: Ma, Jian-Xing
? TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
? TITLE OR INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
? FILE REFERENCE: 5820, 656
? CURRENT FILING DATE: 2004-12-13
? PRIOR APPLICATION NUMBER: 10/963,115
? PRIOR FILING DATE: 2004-10-12
? PRIOR APPLICATION NUMBER: 60/510,620
? PRIOR FILING DATE: 2003-10-10
? PRIOR APPLICATION NUMBER: 60/528,647
? PRIOR FILING DATE: 2003-12-11
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: Patentin version 3.3
? SEQ ID NO 4
? LENGTH: 339
? TYPE: PRT
? ORGANISM: Rhesus monkey
? US-11-010-874-4

```

Query Match	93.6%;	Score 1442;	DB 7;	length 339;
Best Local Similarity	93.1%;	Pred. No. 2.5e-11;		
Matches 242;	Conservative	9;	Mismatches 9;	Indels 0; Gaps 0;

QY	1	YLLSECKTGNKKNYGTMSKTKNGKITQKMSSTSPHRPRFSPATHPSEGLBENYCNPN	60
Db	1	YLLSECKTGNKKNYGTMSKTRGTITQKMSSTSPHRPRFSPATHPSEGLBENYCNPN	60
QY	61	DPOGFWCTTTPPEKRYDYCDLIEGEEBCMGCGENYDGIKSTMSGLBEOAMDSSPHAN	120
Db	61	DGOGWCTTTPPEERFDYCDIPECEDEBCHGSGENYDGIKSTMSGLBEOAMDSSPHAN	120
QY	121	GYISPKFPNNKILKKNYCNPNRELHPWCFTTTPNNKWEICDIPTCTTPPSSGPTQCCLK	180
Db	121	GYISPKFPNNKILKKNYCNPNDEHPWPCTTTPNNKWEICDIPTCTTPPSSGPTQCCLK	180
QY	181	GTGENYRGNVAVTYSGHTCQHWSAOTPHTHEPTPENFCKNIDENYCNPNDGKAPWCHT	240
Db	181	GTGENYRGNVAVTYSGHTCHGWSAOTPHTHNTPENFCKNIDENYCNPNDEGKAPWCHT	240
QY	241	TNSQWRMEYCKIPSCDSSPV 260	
Db	241	TNSQWRMEYCKIPSCSSPV 260	

RESULT 7

```

? Sequence 6, Application US/11010874
? Publication No. US20050250694A1
?
? GENERAL INFORMATION:
? APPLICANT: Ma, Jian-Xing
? TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
? TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
? FILE REFERENCE: 5820, 656
? CURRENT APPLICATION NUMBER: US/11/010,874
? CURRENT FILING DATE: 2004-12-13
? PRIOR APPLICATION NUMBER: 10/963,115
? PRIOR FILING DATE: 2004-10-12
? PRIOR APPLICATION NUMBER: 60/510,620
? PRIOR FILING DATE: 2003-10-10
? PRIOR APPLICATION NUMBER: 60/528,647
? PRIOR FILING DATE: 2003-12-11
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO: 6
? LENGTH: 339
? TYPE: PRT
? ORGANISM: bovine
? US-11-010-874-6

```

Query Match	84.2%;	Score 1296;	DB 7;	Length 339;
Best Local Similarity	81.2%;	Pred. No. 2.2e-99;		
Matches 21;	Conservative 22;	Mismatches 27;	Indels 0;	Gaps 0;

Qy	1	VYLBECRTGNDKNNYRGVTSKTKNGTTCQKMSSTSPHRRPFPSPATHPSEGLEENYCNPN	60
Db	1	LYLLECKTGNGQYTRGTTAETKSGVTCQKMSSTSHVKEFSEKPPLAGLEENYCNPN	60
Qy	61	DPQGPWCYTTDPEKRYDYCDILCEBECMCSGENYDGKISTMSGLECCAMDQSPH	120
Db	61	DENGPWCYTTDPPDKRYDCDIPECEDKCMHSGENYEGKIATKMSGRDCAMDQSPH	120
Qy	121	GYTSKPPNKKLKNYCNPNDRRLAPMCFITDPRNRMELCDIPRCTTPPSSGPYQCL	180
Db	121	GYTSKPPNKKLKNYCNPNDRBPPMCFITDPOQRMECDIPRCTTPPSSGPYQCL	180
Qy	181	GTGENYGNVAVTVSGHTCOHMSAQTPHTHERTPENPFCNLDENYCRNPDGRAPWC	240
Db	181	GTGNVGGTVAVTVSGHTCOHMSBQTPHKHARTPENPFCNLEENYCRNPDGRAPWC	240
Qy	241	TNSQVRMEYCKIPSCDSAPV	260
Db	241	TNSEVRMEYCTIPSCSSPL	260

RESULT 8

Db 338 TDSQLRWEYCEIPSCSS 355

RESULT 11

US-11-010-874-8

; Sequence 8, Application US/11010874
; Publication No. US20050250694A1

; GENERAL INFORMATION:

; APPLICANT: Ma, Jian-Xing

; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND

; FILE REFERENCE: 5820.656

; CURRENT APPLICATION NUMBER: US/11/010,874

; PRIOR FILING DATE: 2004-12-13

; PRIOR APPLICATION NUMBER: 10/963,115

; PRIOR FILING DATE: 2004-10-12

; PRIOR APPLICATION NUMBER: 60/510,620

; PRIOR FILING DATE: 2003-10-10

; PRIOR APPLICATION NUMBER: 60/528,647

; PRIOR FILING DATE: 2003-12-11

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 8

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-010-874-8

Query Match 65.0%; Score 1001; DB 7; Length 168;

Best Local Similarity 99.4%; Pred. No. 1.5e-75;

Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 88 CMHSGENVYDGIKSTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELPRW 147

Db 1 CMHSGENVYDGIKSTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELPRW 60

QY 148 CFTTDPNKRWEICDIPTCTPPSSGPTYQCLKGTGENYRGNAVAVTSGHTCQWMSAOTP 207

Db 61 CFTTDPNKRWEICDIPTCTPPSSGPTYQCLKGTGENYRGNAVAVTSGHTCQWMSAOTP 120

QY 208 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 255

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 168

QY 88 CMHSGENVYDGIKSTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELPRW 147

Db 1 CMHSGENVYDGIKSTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELPRW 60

QY 148 CFTTDPNKRWEICDIPTCTPPSSGPTYQCLKGTGENYRGNAVAVTSGHTCQWMSAOTP 207

Db 61 CFTTDPNKRWEICDIPTCTPPSSGPTYQCLKGTGENYRGNAVAVTSGHTCQWMSAOTP 120

QY 208 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVWEYCKIPSC 255

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

QY 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCCTTNSQVWEYCKIPSC 168

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Rhesus monkey
US-11-010-874-14

Query Match 58.2%; Score 896; DB 7; Length 160;
Best Local Similarity 93.8%; Pred. No. 5.7e-67;
Matches 150; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTGTGKKNYRGITGKTKNGITCOKWSSTSPHRPRSPATHSBGLBENYCRNPNDPQGP 65
DB 1 CTGTGKKNYRGITGKTKNGITCOKWSSTSPHRPRSPATHSBGLBENYCRNPNDPQGP 60
QY 66 WCYTTPERKRYDCILBCEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAGYIPS 125
DB 61 WCYTTPERKRYDCILBCEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAGYIPS 120
QY 126 KFPNKLKKNYCRNPDRRLRPMWCTTDPNKRWELCDIPRC 165
DB 121 KFPNKLKKNYCRNPDRRLRPMWCTTDPNKRWELCDIPRC 160

RESULT 15

US-11-010-874-10
; Sequence 10, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820.656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 168
; TYPE: PRT
; ORGANISM: porcine
US-11-010-874-10

Query Match 57.3%; Score 883; DB 7; Length 168;

Best Local Similarity 84.5%; Pred. No. 6.9e-66;
Matches 142; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 88 CMHSGENYDGIKSTMSGLECOAMDOSPHAGYIPSKFPNKLKKNYCRNPDRRLRPM 147
DB 1 CMHSGENYDGIKSTMSGLECOAMDOSPHAGYIPSKFPNKLKKNYCRNPDRRLRPM 60
QY 148 CFTTDPNKRWELCDIPRCCTTTPPSGPTYQCLKGTGENTRGNAVAVTSGHTCQWMSAQTP 207
DB 61 CFTTDPNKRWELCDIPRCCTTTPPSGPTYQCLKGTGENTRGNAVAVTSGHTCQWMSAQTP 120
QY 208 HTHERTPENPCNULDENYCRNPDKKRAKPCHTTNSQVWREYCKIPSC 255
DB 121 HTHERTPENPCNULDENYCRNPDKKRAKPCHTTNSQVWREYCKIPSC 168

Search completed: January 25, 2006, 17:22:35
Job time : 33 secs

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stjepic M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Teshlyuk S., Carrinck P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RA PROTEIN SEQUENCE OF 20-810, AND VARIANT ASN-472.
 RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
 RA Submitted (JUL-1977) to the PIR data bank.
 [7]
 RA NUCLEOTIDE SEQUENCE OF 292-810.
 RA MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen.";
 RT Biochemistry 23:4243-4250(1984).
 [8]
 RA PROTEIN SEQUENCE OF 20-100.
 RA MEDLINE=75093329; PubMed=122932;
 RA Wiman B., Wallen P.;
 RT "Structural relationship between 'glutamic acid' and 'lysine' forms of
 RT human plasminogen and their interaction with the NH2-terminal
 RT activation peptide as studied by affinity chromatography.";
 RT Eur. J. Biochem. 50:489-494(1975).
 [9]
 RA PROTEIN SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810, AND VARIANT
 RA ASN-472.
 RA Sottrup-Jensen L., Claeyse H., Zajdel M., Petersen T.E., Magnusson S.;
 RT "The primary structure of human plasminogen.";
 RT (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
 RT Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
 RT Raven Press, New York (1978).
 [10]
 RA PROTEIN SEQUENCE OF 483-604.
 RA MEDLINE=76043692; PubMed=126863;
 RA Wiman B., Wallen P.;
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human
 RT plasminogen that forms the linkage between the plasmin chains.";
 RT Eur. J. Biochem. 58:539-547(1975).
 [11]
 RA PROTEIN SEQUENCE OF 581-810.
 RA MEDLINE=77225245; PubMed=142009;
 RA Wiman B.;
 RT "Primary structure of the B-chain of human plasmin.";
 RT Eur. J. Biochem. 76:129-137(1977).
 [12]
 RA ACTIVE SITE.
 RA MEDLINE=73149248; PubMed=4694729;
 RA Robbins K.C., Bernabe P., Arrazon L., Summaria L.;
 RT "The primary structure of human plasminogen. II. The histidine loop of
 RT human plasmin: light (B) chain active center histidine sequence.";
 RT J. Biol. Chem. 248:1631-1633(1973).
 [13]
 RA ACTIVE SITE.
 RA MEDLINE=69234739; PubMed=4240117;
 RA Groskopf W.R., Summaria L., Robbins K.C.;
 RT "Studies on the active center of human plasmin. Partial amino acid
 RT sequence of a peptide containing the active center serine residue.";
 RT J. Biol. Chem. 244:3590-3597(1969).
 [14]
 RA OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
 RA MEDLINE=82213905; PubMed=6919539;

RA Trexler M., Vail Z., Patchy L.;
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human
 RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
 RT binding of ligand by kringle 4.";
 RT J. Biol. Chem. 257:7401-7406(1982).
 [15]
 RA FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
 RA MEDLINE=85054794; PubMed=6094526;
 RA Vail Z., Patchy L.;
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are
 RT essential for fibrin affinity of the kringle 1 domain.";
 RT J. Biol. Chem. 259:13690-13694(1984).
 [16]
 RA PHOSPHORYLATION SITE SER-597.
 RA MEDLINE=97345939; PubMed=9201958; DOI=10.1021/bi970328d;
 RA Wang H., Protok M., Bretthauer R.K., Castellino F.J.;
 RT "Serine-578 is a major phosphorylation locus in human plasma
 RT plasminogen.";
 RT Biochemistry 36:8100-8106(1997).
 [17]
 RA CARBOHYDRATE-LINKAGE SITES.
 RA MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P.,
 RA Gerwig G.J., van Halbeek H., Vilegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.";
 RT Eur. J. Biochem. 173:57-63(1988).
 [18]
 RA CARBOHYDRATE-LINKAGE SITE SER-268.
 RA MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;
 RA Pirte-Shepherd S.R., Stevens R.D., Don N.L., Englund J.J.,
 RA Pizzo S.V.;
 RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
 RT human plasminogen 2.";
 RT J. Biol. Chem. 272:7408-7411(1997).
 [19]
 RA CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.
 RA MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RT Cell 79:315-328(1994).
 [20]
 RA CHARACTERIZATION OF ANGIOSTATIN.
 RA MEDLINE=97238710; PubMed=9102221;
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
 RA Lapevich R., Nacy C.A.;
 RT "A recombinant human angiostatin protein inhibits experimental primary
 RT and metastatic cancer.";
 RT Cancer Res. 57:1329-1334(1997).
 [21]
 RA X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
 RA MEDLINE=92031502; PubMed=1657148;
 RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
 RT "Crystal and molecular structure of human plasminogen kringle 4
 RT refined at 1.9-A resolution.";
 RT Biochemistry 30:10576-10586(1991).
 [22]
 RA X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
 RA MEDLINE=92031503; PubMed=1657149;
 RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
 RT "The refined structure of the epsilon-aminocaproic acid complex of
 RT human plasminogen kringle 4.";
 RT Biochemistry 30:10589-10594(1991).
 [23]
 RA X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
 RA PubMed=15299951; DOI=10.1107/S0907444996012267;
 RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
 RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
 RT A possible structural role of disordered residues.";
 RT Acta Crystallogr. D 53:169-178(1997).

RN [24]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.

Query Match 99.7%; Score 1535; DB 1; Length 810;
Best Local Similarity 99.6%; Pred. No. 2.4e-108;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHPPFPSPATHPSEGLSENYCENPN 60
DB 98 VLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHPPFPSPATHPSEGLSENYCENPN 157
QY 61 DPGFWCYTTDPDEKRYDYCDILECEBECMHGSGENYDGKISKMSGLECOAMDOSPHAH 120
DB 158 DPGFWCYTTDPDEKRYDYCDILECEBECMHGSGENYDGKISKMSGLECOAMDOSPHAH 217
QY 121 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKKMELCDIPRCTPPSSGPTYQCLK 180
DB 218 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKKMELCDIPRCTPPSSGPTYQCLK 277
QY 181 GGENYRGVAATVSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGRAPWCHT 240
DB 278 GGENYRGVAATVSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2

OSTEH4 HUMAN
ID OSTEH4_HUMAN PRELIMINARY; PRT; 810 AA.

AC OSTEH4_1
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Plasminogen.
GN Name=PLG; ORFNames=RPL-81D8.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109933; CAI22908.1; -; Genomic_DNA.
DR SMR; OSTEH4; 562-810.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003609; PAN.
DR InterPro; IPR003609; PAN_app.
DR InterPro; IPR011358; Pept_S1A_Plaamin.
DR InterPro; IPR001254; Peptidase_S1_86.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001150; Plasmin; 1.
DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyse; Kringle; Protease; Repeat; Serine protease.
SQ SEQUENCE 810 AA; 90569 MW; 8B31CB877C3AB6 CRC64;

Query Match 99.7%; Score 1535; DB 2; Length 810;
Best Local Similarity 99.6%; Pred. No. 2.4e-108;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHPPFPSPATHPSEGLSENYCENPN 60
DB 98 VLSECKTGNGKNGYGTMSKTNGITCQKMSSTSPHPPFPSPATHPSEGLSENYCENPN 157
QY 61 DPGFWCYTTDPDEKRYDYCDILECEBECMHGSGENYDGKISKMSGLECOAMDOSPHAH 120
DB 158 DPGFWCYTTDPDEKRYDYCDILECEBECMHGSGENYDGKISKMSGLECOAMDOSPHAH 217
QY 121 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKKMELCDIPRCTPPSSGPTYQCLK 180
DB 218 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKKMELCDIPRCTPPSSGPTYQCLK 277
QY 181 GGENYRGVAATVSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGRAPWCHT 240
DB 278 GGENYRGVAATVSGHTCOHWSAOTPHTHERTPENFPCKNLDENYCRNPDGRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3

Q5R8X6 PONPY
ID Q5R8X6_PONPY PRELIMINARY; PRT; 810 AA.

AC Q5R8X6_1
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp470G2422.
GN Name=DKFZp470G2422;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Pousetka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amd C., Osanger A., Fobio G., Han M., Wilemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CB859622; CNH91784.1; -; mRNA.
DR SMR; Q5R8X6; 185-352; 564-810.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; PAN_app.
DR InterPro; IPR011358; Pept_S1A_Plaamin.
DR InterPro; IPR001254; Peptidase_S1_86.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.

DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00948; PAN; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Hypothetical protein; Kringle; Protease; Repeat;
 KM Serine protease.
 SQ SEQUENCE 810 AA; 90380 MW; 126D530C942ADD4 CRC64;

Query Match 94.7%; Score 1458; DB 2; Length 810;
 Best Local Similarity 95.0%; Pred. No. 1.7e-102;
 Matches 247; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNYRGTMKKTNGITCKQWSTSPHPRPSPATPSBGLSENYCRNPDN 60
 DB 98 VLSCKTGNGKNYRGTMKKTNGITCKQWSTSPHPRPSPATPSBGLSENYCRNPDN 157

QY 61 DPQGPWCYTTDEPKRYDCDILCEBECNHCSENGYDKISKTMSGLCEQANDSQSPH 120
 DB 158 DAQGPWCYTTDEPKRYDCDILCEBECNHCSENGYDKISKTMSGLCEQANDSQSPH 217

QY 121 GYIPSPKPKNKLKRYCGRPDRLRPWCCTTPPNKRMELCDIPRCTPPSSGPTYYQCK 180
 DB 218 GYIPSPKPKNKLKRYCGRPDRLRPWCCTTPPNKRMELCDIPRCTPPSSGPTYYQCK 277

QY 181 GTGENYRGVAATVSGTQCHWSAOTPHHERTPENFPCKNDENYCRPDGKRAPWCHT 240
 DB 278 GTGENYRGVAATVSGTQCHWSAOTPHHERTPENFPCKNDENYCRPDGKRAPWCHT 337

QY 241 TNSQVMEYCKIIPSCDSSPV 260
 DB 338 TNSQVMEYCKIIPSCDSSPV 357

RESULT 4
 PLAN MACMU STANDARD; PRT; 810 AA.
 ID PLAN MACMU STANDARD; PRT; 810 AA.
 AC P12545;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A;
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
 DE chain B].
 GN Name:Plg;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_Taxid=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89174660; PubMed=2925643;
 RA Tomlinson J.E., McLean J.W., Lawn R.M.;
 RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 RT synthesis.",
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian

CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Activated with catalytic amounts of streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-580, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (by similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; J04697; AAA36901.1; -; mRNA.
 CC PIR; B32869; B30848.
 CC HSSP; P00747; 1BUI.
 CC SMR; P12545; 184-352, 564-810.
 CC MEROPS; S01.233; -;
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003014; PAN.
 CC InterPro; IPR003609; Pan app.
 CC InterPro; IPR011358; Pept S1A plasmin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR003966; Peptidase_S1A_pr.
 CC InterPro; IPR003966; Peptidase_S1A.
 CC Pfam; PF00051; Kringle; 5.
 CC Pfam; PF00024; PAN; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PIRSF; PIRSF001150; Plasmin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC PRINTS; PR01505; PROTHROMBIN.
 CC PRODOM; PD000395; Kringle; 5.
 CC SMART; SM00473; PAN; 1.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS00021; KRINGLE_1; 5.
 CC PROSITE; PS00070; KRINGLE_2; 5.
 CC PROSITE; PS00948; PAN; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
 CC Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling;
 CC Zymogen.
 CC KX Zymogen.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 810 Plasminogen.
 CC FT CHAIN 20 580 Plasmin heavy chain A.
 CC FT PEPTIDE 20 96 Activation peptide.
 CC FT CHAIN 97 580 Plasmin heavy chain A, short form.
 CC FT CHAIN 581 810 Plasmin light chain B.
 CC FT DOMAIN 20 98 PAN.
 CC FT DOMAIN 103 181 Kringle 1.
 CC FT DOMAIN 144 262 Kringle 2.
 CC FT DOMAIN 275 352 Kringle 3.
 CC FT DOMAIN 377 454 Kringle 4.

```

FT DOMAIN 481 560 Kringle 5.
FT DOMAIN 581 808 Peptidase S1.
FT ACT_SITE 622 622 Charge relay system.
FT ACT_SITE 665 665 Charge relay system.
FT ACT_SITE 760 760 Charge relay system.
FT BINDING 134 134 Fibrin.
FT BINDING 136 136 Fibrin.
FT BINDING 136 136 Omega-aminocarboxylic acids.
FT BINDING 158 158 Omega-aminocarboxylic acids.
FT BINDING 172 172 Omega-aminocarboxylic acids.
FT BINDING 432 432 Omega-aminocarboxylic acids.
FT BINDING 445 445 Omega-aminocarboxylic acids.
FT CARBOXHD 365 365 O-linked (GalNac. . .) (By similarity).
FT DISULFID 49 73 By similarity.
FT DISULFID 53 61 By similarity.
FT DISULFID 103 181 By similarity.
FT DISULFID 124 164 By similarity.
FT DISULFID 152 176 By similarity.
FT DISULFID 185 262 By similarity.
FT DISULFID 188 316 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 377 454 By similarity.
FT DISULFID 398 437 By similarity.
FT DISULFID 426 449 By similarity.
FT DISULFID 481 560 By similarity.
FT DISULFID 502 543 By similarity.
FT DISULFID 531 555 By similarity.
FT DISULFID 567 685 Interchain (between A and B chains) (By similarity).
FT DISULFID 577 585 Interchain (between A and B chains) (By similarity).
FT DISULFID 607 623 By similarity.
FT DISULFID 699 766 By similarity.
FT DISULFID 729 745 By similarity.
FT DISULFID 756 784 By similarity.
SQ SEQUENCE 810 AA; 90255 MW; A75E1CS1A1A0F24A CRC64;

```

Query Match 93.6%; Score 1442; DB 1; Length 810;
 Best Local Similarity 93.1%; Pred. No. 2.8e-101;
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```

QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRRPSPATHPSBGLSENYCRNP 60
DB 98 VYLSECKTGNGKNGYGTMSKTKRTGTCQKWSSTSPHRRPSPATHPSBGLSENYCRNP 157
QY 61 DPGWCCTTDPBKKYDYCDILCEBECMHGSGENYDGIKSTKMGLECOAWDSOPHAH 120
DB 158 DPGWCCTTDPBKKYDYCDILCEBECMHGSGENYDGIKSTKMGLECOAWDSOPHAH 217
QY 121 GYIPSKFPKMKLKNKYCNPDRLELPPWCFTTDPNKRKMLCDIPRCTPPSPSGPTTQCLK 180
DB 218 GYIPSKFPKMKLKNKYCNPDRLELPPWCFTTDPNKRKMLCDIPRCTPPSPSGPTTQCLK 277
QY 161 GTGENYRGNAVTVSGHTCQKWSAQTPTHTERTPENPCKNLDENYCRNPDKRAPWC 240
DB 278 GTGENYRGNAVTVSGHTCQKWSAQTPTHTERTPENPCKNLDENYCRNPDKRAPWC 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

```

RESULT 5
 Q8WNR1_CANFA PRELIMINARY; PRT; 359 AA.
 AC Q8WNR1;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

```

DE Plaeminogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Placentalia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pirie-Shepherd S.R., Coffman K.T., Reenick D., Chan R., Kisker O.,
RA Folkman J., Waters D.J.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069985; AAL8519.1; -, mRNA.
DR HSSP; P00747; 1PMK.
DR SMR; Q8WNR1; 87-255.
DR Ensembl; ENSCAF0000000759; Canis familiaris.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringle; 4.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
FT Kringle.
FT NON_TER 1 1
FT NON_TER 359 359
SQ SEQUENCE 359 AA; 41172 MW; 776D35F4AB0BD98 CRC64;

```

Query Match 84.8%; Score 1306; DB 2; Length 359;
 Best Local Similarity 81.2%; Pred. No. 2.6e-91;
 Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

```

QY 1 VYLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRRPSPATHPSBGLSENYCRNP 60
DB 1 VYLSECKTGNGKNGYGTMAKTNDVACQKWSNDSHPKDPYPERKPLBGLSENYCRNP 60
QY 61 DPGWCCTTDPBKKYDYCDILCEBECMHGSGENYDGIKSTKMGLECOAWDSOPHAH 120
DB 61 DPGWCCTTDPBKKYDYCDILCEBECMHGSGENYDGIKSTKMGLECOAWDSOPHAH 120
QY 121 GYIPSKFPKMKLKNKYCNPDRLELPPWCFTTDPNKRKMLCDIPRCTPPSPSGPTTQCLK 180
DB 121 GYIPSKFPKMKLKNKYCNPDRLELPPWCFTTDPNKRKMLCDIPRCTPPSPSGPTTQCLK 180
QY 161 GTGENYRGNAVTVSGHTCQKWSAQTPTHTERTPENPCKNLDENYCRNPDKRAPWC 240
DB 161 GGBESYRKSVSTVSGHTCQKWSAQTPTHTERTPENPCKNLDENYCRNPDKRAPWC 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

```

RESULT 6
 PLMN_RAT STANDARD; PRT; 812 AA.
 AC Q01177; Q8ROW3; (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plaeminogen precursor (BC 3.4.21.7) (Contains: Plaemin heavy chain A;
 DE Activation peptide; Angiotensin; Plaemin heavy chain A, short form;
 DE Plaemin light chain B).
 GN Name=Pig;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.

OK NCBI_TaxID=10116;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RC TISSUE: Liver;
 RA Bangert K.; Johnsen A.H.; Thorsen S.;
 RA "Rat plasminogen: cDNA and gene structure."
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RC NUCLEOTIDE SEQUENCE OF 343-511.
 RC TISSUE: Liver;
 RC MEDLINE=91250378; PubMed=1645711;
 RA Kanaias J.J.; Macker S.P.;
 RA "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RT receptor site for plasminogen."
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -1- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks
 CC neovascularization and growth of experimental primary and
 CC metastatic tumors in vivo (By similarity).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-581, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (By similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clots.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AJ242649; CAB46014.1; -; mRNA.
 DR EMBL; M62832; AAA41884.1; -; mRNA.
 DR PIR; A40522; A40522.
 DR HSSP; P00747; 1PMK.
 DR SMR; O01177; 565-812.
 DR MEROPS; S01.233; -.
 DR Ensembl; ENSRNOG0000017223; Rattus norvegicus.
 DR RGD; 619893; Pig.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR011358; Pept_S1A_plasmin.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR Pfam; PF000051; Kringle; 5.
 DR Pfam; PF00004; PAN; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.

DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Fibrinolysis; Hydrolyase; Kringle; Plasma; Protease;
 KW Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 FT SIGNAL 1
 FT CHAIN 19
 FT CHAIN 20
 FT CHAIN 20
 FT PEPTIDE 20
 FT CHAIN 98
 FT CHAIN 98
 FT CHAIN 98
 FT CHAIN 582
 FT CHAIN 20
 FT DOMAIN 102
 FT DOMAIN 184
 FT DOMAIN 274
 FT DOMAIN 375
 FT DOMAIN 480
 FT DOMAIN 582
 FT ACT_SITE 624
 FT ACT_SITE 667
 FT ACT_SITE 667
 FT ACT_SITE 762
 FT DISULFID 49
 FT DISULFID 53
 FT DISULFID 103
 FT DISULFID 124
 FT DISULFID 152
 FT DISULFID 185
 FT DISULFID 206
 FT DISULFID 234
 FT DISULFID 275
 FT DISULFID 296
 FT DISULFID 324
 FT DISULFID 347
 FT DISULFID 376
 FT DISULFID 397
 FT DISULFID 425
 FT DISULFID 449
 FT DISULFID 481
 FT DISULFID 502
 FT DISULFID 531
 FT DISULFID 568
 FT DISULFID 578
 FT DISULFID 609
 FT DISULFID 701
 FT DISULFID 721
 FT DISULFID 758
 FT CONFLICT 418
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410EBC9E CRC64;
 Query Match 84.4%; Score 1299; DB 1; Length 812;
 Best Local Similarity 82.6%; Pred. No. 2, 1e-90;
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGKNGVGTMSKTNGITCQMSSTSPHRRPSPATPPSGLSENYCRNPDN 60
 DB 98 VYLSECKTGNGKNGVGTMSKTNGITCQMSSTSPHRRPSPATPPSGLSENYCRNPDN 157
 QY 61 DPQGWGCTTTPDEKRYDYCDLIECEBCHGSGENYDGIKSTMSGLSCQANDSGSPAH 120
 DB 158 DEQGWGCTTTPDQRYEYCNIPCEBCHGSGENYDGIKSTMSGLSCQANDSGSPAH 217
 QY 121 GYIPKFPKNTKKNYCRNPDELRPWCTTDPNKRWELCDIPRCTTPPSGPTQCLK 180
 DB 218 GYIPKFPKNTKKNYCRNPDELRPWCTTDPNKRWELCDIPRCTTPPSGPTQCLK 277

QY 181 GTGNGYRGNAVTVSGHTCOHWSAOTPHRTERTPENPCKNLDENYCRNPDGRAPWCHT 240
 DB 278 GGGNGYRGVSTYASGKTQCRWSSEQTPRHNNTPENPCKNLENNYCRNPDELTAPWCTT 337
 QY 241 TNSQVRWEYCKIPSCDSS 258
 DB 338 TDSQLRWEYCEIPSCGSS 355

RESULT 7
 QSBK6_RAT
 ID QSBK6_RAT PRELIMINARY; PRT; 812 AA.
 AC QSBK6;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Plg protein.
 GN Name=Plg;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 NC NCB1_Taxid=10116;
 [1]
 NUCLEOTIDE SEQUENCE.
 RP TISSUE=Liver;
 RC MEDLINE=2228857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.O., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.A., McGowan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 NUCLEOTIDE SEQUENCE.
 RP TISSUE=Liver;
 RC NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC091133; AAH91135.1; -; mRNA.
 DR SMR; QSBK6; 565-812.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004283; F:plasmin activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR GO; GO:0005874; P:organismal physiological process; IEA.
 DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000001; Kringles.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR011358; Pept_SIA_plasmin.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR Pfam; PF00051; Kingle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Kringles; Protease; Repeat; Serine protease.
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410B8C9E CRC64;

Query Match 84.4%; Score 1299; DB 2; Length 812;
 Best Local Similarity 82.6%; Pred. No. 2.1e-90;
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNGYCKTNGKITCOKMSSTSPHRRPSPATPSBGLSENYCRNPDN 60
 DB 98 VLSCKTGIGKYGKTSKTKTGVTGVCQKMSDTSHPVPTSPSTPSBGLSENYCRNPDN 157

QY 61 DPGPCWCTTDPPEKRYDCDILECEEBCWMCSENYDCKISKTMSGLBCQAMDSQSPHAN 120
 DB 158 DPGPCWCTTDPDQRYEYCNIPCEBECMYCGEYKSGKISTMSGLDQMSDQSPHAN 217

QY 121 GYIPKFPKNIKKNYCRNPDELRPPWCFTTDPNKRWEICDIPRCTTPPSSGPTQCLK 180
 DB 218 GYIPKFPKSNKKNYCRNPDELRPPWCFTTDPNKRWEICDIPRCTTPPSSGPTQCLK 277

QY 181 GTGNGYRGNAVTVSGHTCOHWSAOTPHRTERTPENPCKNLDENYCRNPDGRAPWCHT 240
 DB 278 GGGNGYRGVSTYASGKTQCRWSSEQTPRHNNTPENPCKNLENNYCRNPDELTAPWCTT 337

QY 241 TNSQVRWEYCKIPSCDSS 258
 DB 338 TDSQLRWEYCEIPSCGSS 355

RESULT 8
 PLMN_PIG
 ID PLMN_PIG STANDARD; PRT; 790 AA.
 AC P06867;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (BC 3.4.21.7) [Contains: Plasmin heavy chain A;
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
 DE chain B].
 GN Name=Plg;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 NC NCB1_Taxid=9823;
 [1]
 PROTEIN SEQUENCE OF 1-560.
 RP Schaller J., Marti T., Roeseleat S.J., Kaempfer U., Rickli B.E.;
 RA "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 of the carbohydrate attachment sites with the human and bovine
 species";
 RT Fibrinolysis 1:91-102(1987).
 RL [2]
 PROTEIN SEQUENCE OF 450-790.
 RP MEDLINE=85203907; PubMed=3846533;
 RA Marti T., Schaller J., Rickli B.E.;
 RT "Determination of the complete amino-acid sequence of porcine
 miniplasminogen";
 RL Eur. J. Biochem. 149:279-285 (1985).
 [3]
 CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=88185329; PubMed=3356193;

RA Marti T., Schaller J., Rickli E.E., Schmid K., Kameiling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenthart J.F.,
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to stalylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
CC -1- FUNCTION: plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion, and
CC inflammation; in ovulation it weakens the walls of the Graafian
CC follicle. It activates the urokinase-type plasminogen activator,
CC collagenases and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC Wilbrand factor.
CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Cannot be activated with streptokinase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: N-linked glycan contains N-acetylglucosamine, sialic acid and
CC is core fucosylated. O-linked glycans consist of Gal-GalNAc
CC disaccharide which is modified with up to 2 sialic acid residues
CC (microheterogeneity).
CC -1- PTM: In the presence of the inhibitor, the activation involves
CC only cleavage after Arg-560, yielding two chains held together by
CC two disulfide bonds. In the absence of the inhibitor, the
CC activation involves additionally the removal of the activation
CC peptide (by similarity).
CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC subfamily.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -1- SIMILARITY: Contains 1 PAN domain.
CC -1- SIMILARITY: Contains 1 peptidase S1 domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on ite-
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR PIR, S03733; PLPG.
DR HSP, P00747, 1BU1.
DR SMR, P06867, 544-790.
DR MEROPS, S01.233;
DR GLYcosultcDB; P06867;
DR InterPro; IPR000001, Kringle.
DR InterPro; IPR003014, PAN.
DR InterPro; IPR003609, Pan app.
DR InterPro; IPR011350, Pept_S1A.plasmin.
DR InterPro; IPR001254, Peptidase_S1_Sc.
DR InterPro; IPR003114, Peptidase_S1A.
DR InterPro; IPR003966, Peptidase_S1A_pr.
DR Pfam; PF00051, Kringle; 5.
DR Pfam; PF00024, PAN; 1.
DR Pfam; PF00089, Trypsin; 1.
DR PIRSF; PIRSF001150, Plasmin; 1.
DR PRINTS; PR00722, CHYMOTRYPSIN.
DR PRINTS; PR00018, KRINGLE.
DR PRINTS; PR01505, PROTHROMBIN.
DR ProDom; PD000395, Kringle; 5.
DR SMART; SMO0130, KR; 5.
DR SMART; SMO0473, PAN_Ap; 1.
DR SMART; SMO0020, TRY_Spc; 1.
DR PROSITE; PS00021, KRINGLE_1; 5.
DR PROSITE; PS50070, KRINGLE_2; 5.
DR PROSITE; PS50948, PAN; 1.
DR PROSITE; PS50240, TRYPSIN_DOM; 1.
DR PROSITE; PS00134, TRYPSIN_HIS_FALSE_NRG.
DR PROSITE; PS00135, TRYPSIN_SER; 1.

KM	Blood coagulation; Direct protein sequencing; Fibrinolysis;
KM	Glycoprotein; Hydrolyase; Kringler; Plasma; Protease; Repeat;
KW	Serine protease; Tissue remodeling; Zymogen.
FT	CHAIN 1 560
FT	PEPTIDE 1 78
FT	CHAIN 79 560
FT	CHAIN 561 790
FT	CHAIN 1 79
FT	DOMAIN 84 162
FT	DOMAIN 166 243
FT	DOMAIN 256 333
FT	DOMAIN 358 435
FT	DOMAIN 461 540
FT	DOMAIN 561 788
FT	ACT_SITE 602 602
FT	ACT_SITE 645 645
FT	ACT_SITE 740 740
FT	CARBOND 289 289
FT	CARBOND 340 340
FT	DISULFID 30 54
FT	DISULFID 34 42
FT	DISULFID 84 162
FT	DISULFID 105 145
FT	DISULFID 133 157
FT	DISULFID 166 243
FT	DISULFID 169 297
FT	DISULFID 187 226
FT	DISULFID 215 238
FT	DISULFID 256 333
FT	DISULFID 277 316
FT	DISULFID 305 328
FT	DISULFID 358 435
FT	DISULFID 379 418
FT	DISULFID 407 430
FT	DISULFID 461 540
FT	DISULFID 482 523
FT	DISULFID 511 535
FT	DISULFID 547 665
FT	DISULFID 557 565
FT	DISULFID 587 603
FT	DISULFID 679 746
FT	DISULFID 709 725
FT	DISULFID 736 764
SQ	SEQUENCE 790 AA; 88593 MW; F04EA06E74BCD58E CRC64;

Query Match	83.9%	Score 1292	DB 1	Length 790
Best Local Similarity	81.4%	Pred. No. 7,1e-90		
Matches	210	Conservative	23	Mismatches 25; Indels 0; Gaps 0
Qy	1	VYLSCKTGNGKNGKNGTWSKTKNGJTCQKWSSTSPHRPRFSPATHPSBGLBENTYCRANDN	60	
Db	79	YILSCKTGNGKNGKNGTTSKTSKSGVTCQKMSVSPHIFKPSBKEPPLAGLBENTYCRANDN	138	
Qy	61	DPOGWCCTTTPBKKYDYCDILCEGECBCHGSGENYDOKISWTWSGLECOAMDQSPHAA	120	
Db	139	DKRGWCCTTTPBETPFYCDIPCEBCEBCHGSGENYBESKISWTWSGLICQKMSGSPHAA	198	
Qy	121	GYPSPKFPKNKKNKYNCRNPDRRLPWCFTTDPNKRWELCDIPRCTTTPPSSGPTYYCLK	180	
Db	199	GILPKFPKNKKNKYNCRNPDRPWPCTTDPDNKRWFCDIPRCTTTPPTSGPTYYCLK	258	
Qy	181	GTEGNRGNAVTVSGHTCQKWSAOTPRTHERTPENFPCKUIDENYCRNPDRKAPFWCHT	240	
Db	259	GGEENYRGVSVYTAGHTCQKWSAOSPKNHNTPENFPCKULBENTYCRNPDRGTAPWCYT	318	
Qy	241	TNSQVWMEYCKIPSCDS	258	
Db	319	TDSVAMDIKCLPSCGS	336	

RESULT 9
 PLMN BOVIN STANDARD: PRT; 812 AA.
 AC P06868; Q28162;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [contains: Plasmin heavy chain A, Activation peptide; Plasmin heavy chain A, short form; Plasmin light chain B].
 OS Name=PLG;
 GN Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA."; Int. Dairy J. 5:593-603(1995).
 RL [2]
 RP PROTEIN SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; PubMed=3846532;
 RA Schaller J., Moser P.W., Danneberger-Muller G.A.K., Rosselet S.J., Kamper U., Rickli E.B.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with human plasminogen.";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 706-812.
 RX MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.B., Schmid K., Kamerling J.P., Riegwig G.J., Van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: N-linked glycan contains N-acetylglucosamine and sialic acid. O-linked glycans consist of Gal-GalNAc disaccharide which is modified with up to 2 sialic acid residues (microheterogeneity).
 CC -1- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-583, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (By similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen

CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; X79402; CAA55939.1; -; mRNA.
 CC EMBL; X02935; AAA30714.1; -; mRNA.
 CC PIR; S45046; PLBO.
 CC HSP; P00747; 2PK4.
 CC SMR; P06868; 191-359, 568-812.
 CC MEROPS; S01.233; -;
 CC GlycoSuiteDB; P06868; -;
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003014; PAN.
 CC InterPro; IPR003609; Pan_app.
 CC InterPro; IPR011358; Pept_S1A_plasmin.
 CC InterPro; IPR001254; Peptidase_S1_S6.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR003966; Peptidase_S1A_pr.
 CC Pfam; PF00051; Kringle; 5.
 CC Pfam; PF00024; PAN; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PIRSF; PIRSF001150; Plasmin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC PRINTS; PR01505; BROTHROMBIN.
 CC ProDom; PD000395; Kringle; 5.
 CC PROSITE; PS00021; KRINGLE_1; 5.
 CC PROSITE; PS50070; KRINGLE_2; 5.
 CC PROSITE; PS50948; PAN; 1.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Direct protein sequencing; Fibrinolysis; KW Glycoprotein; Hydrolyase; Kringle; Plasma; Protease; Repeat; KW Serine protease; Signal; Tissue remodeling; Zymogen.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 812 Plasminogen.
 CC FT CHAIN 27 883 Plasmin heavy chain A.
 CC FT PEPTIDE 27 104 Activation peptide (By similarity).
 CC FT CHAIN 105 583 Plasmin heavy chain A, short form (By similarity).
 CC FT CHAIN 584 812 Plasmin light chain B.
 CC FT DOMAIN 29 105 PAN.
 CC FT DOMAIN 110 188 Kringle 1.
 CC FT DOMAIN 192 269 Kringle 2.
 CC FT DOMAIN 282 359 Kringle 3.
 CC FT DOMAIN 384 461 Kringle 4.
 CC FT DOMAIN 485 564 Kringle 5.
 CC FT DOMAIN 584 810 Peptidase S1.
 CC FT ACT_SITE 624 624 Charge relay system.
 CC FT ACT_SITE 667 667 Charge relay system.
 CC FT ACT_SITE 762 762 Charge relay system.
 CC FT CARBOHYD 315 315 N-linked (GlcNAc...).
 CC FT CARBOHYD 315 315 /FTId=CAR_000014.
 CC FT CARBOHYD 365 365 O-linked (GalNAc...).
 CC FT DISULFID 56 80 /FTId=CAR_000015.
 CC FT DISULFID 60 80 By similarity.
 CC FT DISULFID 110 188 By similarity.
 CC FT DISULFID 131 171 By similarity.
 CC FT DISULFID 159 183 By similarity.
 CC FT DISULFID 182 269 By similarity.
 CC FT DISULFID 195 323 By similarity.
 CC FT DISULFID 213 252 By similarity.
 CC FT DISULFID 241 264 By similarity.
 CC FT DISULFID 282 359 By similarity.

RA Nagaraja R.;
 RT "Genomic sequence analysis in the mouse t-complex region."
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Liver;
 RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altchul S.F., Moore B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
 RA Bosak S.A., Medwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny K.C., Harte S., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN NUCLEOTIDE SEQUENCE OF 1-16.
 RP STRAIN=129/SvJ; TISSUE=Liver;
 RX MEDLINE=22254843; PubMed=12149246; DOI=10.1074/jbc.M202509200;
 RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
 RA Farmer R.J., Miles L.A.;
 RT "Localization of regulatory elements mediating constitutive and
 cytokine-stimulated plasminogen gene expression.";
 RL J. Biol. Chem. 277:38579-38588(2002).
 RN [5]
 RN CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.
 RP MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(95)90200-3;
 RX O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RT Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328(1994).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 a proteolytic factor in a variety of other processes including
 embryonic development, tissue remodeling, tumor invasion, and
 inflammation; in ovulation it weakens the walls of the Graafian
 follicle. It activates the urokinase-type plasminogen activator,
 collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Wilbrand factor.
 CC -1- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks
 CC neovascularization and growth of experimental primary and
 CC metastatic tumors in vivo.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-581, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (By similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.

CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL J04766; AAA50168.1; -; mRNA.
 CC EMBL AF481053; AAM2156.1; -; Genomic_DNA.
 CC EMBL BC014773; AAH14773.1; -; mRNA.
 CC EMBL BC057186; AAH57186.1; -; mRNA.
 CC EMBL AY134430; AAN15805.1; -; Genomic_DNA.
 CC PIR: A38514; PIMS.
 CC HSSP: P00747; 1BUI.
 CC SMR: P20918; 184-352, 566-812.
 CC MEROPS: S01.233; -.
 CC Ensembl: ENSMOTG0000059481; Mus musculus.
 CC MGI: MGI:97620; Plg.
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0006915; P:apoptosis; IDA.
 CC GO: GO:0006917; P:induction of apoptosis; IDA.
 CC GO: GO:0046716; P:muscle maintenance; IMP.
 CC GO: GO:0007519; P:myogenesis; IMP.
 CC GO: GO:0016525; P:negative regulation of angiogenesis; TAS.
 CC GO: GO:0042246; P:tissue regeneration; IMP.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR003014; PAN.
 CC InterPro: IPR003609; Pan_app.
 CC InterPro: IPR011358; Pept_S1A_Plasmin.
 CC InterPro: IPR001254; Peptidase_S1_S6.
 CC InterPro: IPR001314; Peptidase_S1A.
 CC InterPro: IPR003966; Peptidase_S1A_pr.
 CC Pfam: PF00051; Kringle; 5.
 CC Pfam: PF00024; PAN; 1.
 CC Pfam: PF00089; Trypsin; 1.
 CC PIRSF: PIRSF001150; Plasmin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR0018; KRINGLE.
 CC PRINTS: PR01505; PROTHROMBIN.
 CC ProDom: PD000395; Kringle; 5.
 CC PROSITE: PS00021; KRINGLE_1; 5.
 CC PROSITE: PS50070; KRINGLE_2; 5.
 CC PROSITE: PS50948; PAN; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 CC Kringle; Plasma; Precase; Repeat; Serine protease; Signal;
 CC Tissue remodeling; Zymogen.
 CC SIGNAL 1
 CC FT CHAIN 20 812 Plasminogen.
 CC FT CHAIN 20 581 Plasmin heavy chain A.
 CC FT PEPTIDE 20 97 Activation peptide.
 CC FT CHAIN 98 581 Plasmin heavy chain A, short form.
 CC FT CHAIN 98 7436 Angiostatin.
 CC FT CHAIN 582 812 Plasmin light chain B.
 CC FT DOMAIN 20 98 PAN.
 CC FT DOMAIN 103 181 Kringle 1.
 CC FT DOMAIN 184 262 Kringle 2.
 CC FT DOMAIN 275 352 Kringle 3.
 CC FT DOMAIN 377 454 Kringle 4.
 CC FT DOMAIN 481 560 Kringle 5.
 CC FT DOMAIN 582 810 Peptidase S1.
 CC FT ACT_SITE 624 624 Charge relay system (By similarity).
 CC FT ACT_SITE 667 667 Charge relay system (By similarity).
 CC FT ACT_SITE 762 762 Charge relay system (By similarity).
 CC FT DISULFID 49 73 By similarity.
 CC FT DISULFID 53 61 By similarity.
 CC FT DISULFID 103 181 By similarity.
 CC FT DISULFID 124 164 By similarity.
 CC FT DISULFID 152 176 By similarity.
 CC FT DISULFID 185 262 By similarity.

```

FT DISULFID 188 316 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 377 454 By similarity.
FT DISULFID 398 437 By similarity.
FT DISULFID 426 449 By similarity.
FT DISULFID 481 560 By similarity.
FT DISULFID 502 543 By similarity.
FT DISULFID 531 555 By similarity.
FT DISULFID 568 687 Interchain (between A and B chains) (By
FT DISULFID 578 586 similarity).
FT DISULFID 609 625 Interchain (between A and B chains) (By
FT DISULFID 701 768 similarity).
FT DISULFID 731 747 By similarity.
FT DISULFID 758 786 By similarity.
FT CONFLICT 225 235 R -> H (in Ref. 1).
FT CONFLICT 525 525 G -> D (in Ref. 1).
FT CONFLICT 649 649 S -> L (in Ref. 1).
SQ SEQUENCE 812 AA; 90782 MW; 241732606A2FFD2 CRC64;

Query Match 83.1%; Score 1279; DB 1; Length 812;
Beet Local Similarity 81.0%; Pred. No. 7, 1e-89;
Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

QY 1 VLSSECKTGNGKNGYGTMSKTKNGITCKQMSSTSPHPRFSPATPSSEGLEENYCRNPDN 60
DB 98 VLSSECKTGNGKNGYGTMSKTKNGITCKQMSSTSPHPRFSPATPSSEGLEENYCRNPDN 157
QY 61 DPGGWCCTTDDPKRYDYCDIIECEBECMHGCGENTDGKISTKNGSLBQANDSQSPH 120
DB 158 DPGGWCCTTDDPKRYDYCDIIECEBECMHGCGENTDGKISTKNGSLBQANDSQSPH 217
QY 121 GYTPKFPKKNKKYKNCRNPRDLRPMWCTTDPNKRWEICDIIPRCTPPSPSGPTVQCL 180
DB 218 GYTPKFPKKNKKYKNCRNPRDLRPMWCTTDPNKRWEICDIIPRCTPPSPSGPTVQCL 277
QY 181 GTGENYRGNAVTVSGTCHQMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPMCHT 240
DB 278 GTGENYRGNAVTVSGTCHQMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPMCHT 337
QY 241 TNSQVMEYCKIPSCDS 258
DB 338 TDSQLRMEYCEIIPSCSS 355

RESULT 12
PLMN ERIEU STANDARD; PRT; 810 AA.
AC 029485;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A,
DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
DE chain B].
GN Name=Plg;
OS Etrineaeus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
OC Erinaceinae; Erinaceus.
OC NCBI_TaxID=9365;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96055778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;
RA Lawn R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RA Byrne C.D., Fong K.J., Meer K., Patchy L.;
"the recurring evolution of lipoprotein(a). Insights from cloning of

```

```

RT hedgehog apolipoprotein(a).";
RL J. Biol. Chem. 270:24004-24009 (1995).
RN [2]
RP SEQUENCE REVISION.
RA Lawn R.M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion, and
CC inflammation; in ovulation it weakens the walls of the Graafian
CC follicle. It activates the urokinase-type plasminogen activator,
CC collagenase and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC Willibrand factor.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Cannot be activated with streptokinase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: In the presence of the inhibitor, the activation involves
CC only cleavage after Arg-582, yielding two chains held together by
CC two disulfide bonds. In the absence of the inhibitor, the
CC activation involves additionally the removal of the activation
CC peptide (By similarity).
CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC subfamily.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -1- SIMILARITY: Contains 1 PAN domain.
CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U33171, AAC48717.1; -, mRNA.
CC PIR: I46260; I46260.
CC HSSP: P00747; 1B01.
CC SMR: Q29485; 568-810.
CC MEROPS: S01.233; -.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003014; PAN.
CC InterPro: IPR003609; Pan_app.
CC InterPro: IPR01358; Pept_S1A_Plasmin.
CC InterPro: IPR001254; Peptidase_S1_S6.
CC InterPro: IPR001314; Peptidase_S1A.
CC InterPro: IPR003966; Peptidase_S1A_pr.
CC Pfam: PF00051; Kringle; 5.
CC Pfam: PF00024; PAN; 1.
CC Pfam: PF00089; Trypsin; 1.
CC PIRSF: PIRSF001150; Plasmin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC ProDom: PD000395; Kringle; 5.
CC SMART: SM00130; KR; 5.
CC SMART: SM00473; PAN_AP; 1.
CC SMART: SM00020; TRYD_SPC; 1.
CC PROSITE: PS00021; KRINGLE_1; 5.
CC PROSITE: PS50070; KRINGLE_2; 5.
CC PROSITE: PS50948; PAN; 1.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
CC Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling;
CC Zymogen.
FT SIGNAL 1 19 By similarity.

```

FT	CHAIN	20	810	Plasminogen.
FT	CHAIN	20	582	Plasmin heavy chain A (By similarity).
FT	PEPTIDE	20	97	Activation peptide (By similarity).
FT	CHAIN	98	582	Plasmin heavy chain A, short form (By similarity).
FT	CHAIN	583	810	Plasmin light chain B (By similarity).
FT	DOMAIN	20	98	PMN.
FT	DOMAIN	103	181	Kingle 1.
FT	DOMAIN	185	262	Kingle 2.
FT	DOMAIN	275	352	Kingle 3.
FT	DOMAIN	379	456	Kingle 4.
FT	DOMAIN	482	561	Kingle 5.
FT	DOMAIN	582	808	Peptidase S1.
FT	ACT_SITE	622	622	Charge relay system.
FT	ACT_SITE	665	665	Charge relay system.
FT	ACT_SITE	760	760	Charge relay system.
FT	CAROHYD	339	339	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	49	73	By similarity.
FT	DISULFID	53	61	By similarity.
FT	DISULFID	103	181	By similarity.
FT	DISULFID	124	164	By similarity.
FT	DISULFID	152	176	By similarity.
FT	DISULFID	185	262	By similarity.
FT	DISULFID	188	316	By similarity.
FT	DISULFID	206	245	By similarity.
FT	DISULFID	234	257	By similarity.
FT	DISULFID	275	352	By similarity.
FT	DISULFID	326	335	By similarity.
FT	DISULFID	324	347	By similarity.
FT	DISULFID	379	456	By similarity.
FT	DISULFID	400	439	By similarity.
FT	DISULFID	428	451	By similarity.
FT	DISULFID	482	561	By similarity.
FT	DISULFID	503	544	By similarity.
FT	DISULFID	532	556	By similarity.
FT	DISULFID	569	665	Interchain (between A and B chains) (By similarity).
FT	DISULFID	579	586	Interchain (between A and B chains) (By similarity).
FT	DISULFID	607	623	By similarity.
FT	DISULFID	699	766	By similarity.
FT	DISULFID	729	745	By similarity.
FT	DISULFID	756	784	By similarity.
SQ	SEQUENCE	810 AA;	90902 MR;	8E7578094601A16 CRC64;

	Query Match	80.3%;	Score 1237;	DB 1;	Length 810;
	Best Local Similarity	77.9%;	Pred. No. 1.le-85;		
	Matched 201;	Conservative 26;	Mismatches 31;	Indels 0;	Gaps 0.
Qy	1	VYLSCKTNGKNGKYRGTMSKTNGTGTCQKMSSTSPHRRPSPATPSGEGLEENYCRRNDN	60		
Dd	98	MYLSCCKANGNKYYIGTVSKTGTGLCQKMSLETPHKPFSDENPSBELDNYCRANDN	157		
Qy	61	DPOGWCTTTDPKKRYDYCDILACEEBCWHSGSENYDGKISKTMSGLECOAWDSOPHAH	120		
Dd	158	DPKGWCTMTMBEVAYREYCEIITGCDEBCHCGGYVVKISTMSGLECGPWDSQIPHPH	217		
Qy	121	GIYPSKFPFNKLKNKYCRNPDRRLRPWCFTTDPNKRMLCDIPRCTTPPPSSGPTYOCLK	180		
Dd	218	GPIPSKFPSPKLNKNKYCRNPDPGRPRPWCFTMDNRNKRWECDIPRCTTPPPSGPTYOCLM	277		
Qy	181	GTGENYRGNAVAVTSGHTCCQKWSAOTPRTHERTPENFPCKNLDENYICRNPDGKRAPWCHT	240		
Dd	278	GNGEHYQCNVAATVATSGLTQRKEGDSPPHRHDRTPENPYCKNLDENYICRNPDGPAPWCFT	337		
Qy	241	TNSQVRMEYCKIPSCDSS	258		
Dd	338	TNSSVRMEFCIKIPDCVSS	355		
RESULT 13					
ID	Q7TP84_RAT	PRELIMINARY;	PRT	759	AA.

AC	Q77P84; 01-OCT-2003 (TREMBlrel. 25, Created)
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE	Abi-346.
DR	
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridea; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma H.,
RA	Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA	Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY325159; AAP92560.1; -; mRNA.
DR	HSSP; P00747; IBI.
DR	SRP; Q77P84; 83-360, 661-759.
DR	Ensembl; ENSNRG0000017223; Rattus norvegicus.
DR	GO; GO:0005509; F:calcium ion binding; IEA.
DR	GO; GO:0008233; F:peptidase activity; IEA.
DR	GO; GO:0003809; F:thrombin activity; IEA.
DR	GO; GO:0004295; F:trypsin activity; IEA.
DR	GO; GO:0007596; F:blood coagulation; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR000001; Kringle.
DR	InterPro; IPR003014; PAN.
DR	InterPro; IPR01358; Pept_S1A_Plasmin.
DR	InterPro; IPR001254; peptidase_s1_s6.
DR	InterPro; IPR003966; peptidase_S1A_pr.
DR	Pfam; PF00051; Kringle; 5.
DR	Pfam; PF00024; PAN; 1.
DR	PIRSP; PIRSF001150; Plasmin; 1.
DR	PRINTS; PRO0018; KRINGLE.
DR	PRINTS; PRO1505; PROTHROMBIN.
DR	ProDom; PD000395; Kringle; 5.
DR	SMART; SM00130; KR; 5.
DR	SMART; SM00020; TRYD_SPC; 1.
DR	PROSITE; PS00021; KRINGLE_1; 5.
DR	PROSITE; PS00070; KRINGLE_2; 5.
DR	PROSITE; PS02403; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
SO	SEQUENCE 759 AA; 86057 MW; 1422BFAC05C6DPA7 CRC64;

[illegible]

AC 018783; 25-OCT-2004 (Rel. 45, Last Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (BC 3.4.21.7) [Contains: Plasmin heavy chain A,
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
 DE chain B].
 GN Name:Plg;
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=98004511, PubMed=9342350, DOI=10.1073/pnas.94.22.11992;
 RA Lamm R.M., Schwartz K., Patchy L.;
 RT *Convergent evolution of apolipoprotein(a) in primates and hedgehog.;
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 a proteolytic factor in a variety of other processes including
 embryonic development, tissue remodeling, tumor invasion, and
 inflammation; in ovulation it weakens the walls of the Graafian
 follicle. It activates the urokinase-type plasminogen activator,
 collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 Willebrand factor. (By similarity).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 activators, both plasminogen and its activator being bound to
 fibrin. Activated with catalytic amounts of streptokinase (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 only cleavage after Arg-576, yielding two chains held together by
 two disulfide bonds. In the absence of the inhibitor, the
 activation involves additionally the removal of the activation
 peptide (By similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 immediately after dissociation from the clot (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AF012297; AAB65760.1; -; mRNA.
 DR HSSP: P00747; 1BU1.
 DR SMK: O18783; 561-806.
 DR MEROPS: S01.233; -.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; PAN app.
 DR InterPro: IPR011358; Pept_S1A_plasmin.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR003966; Peptidase_S1A_pr.
 DR Pfam: PF00051; Kringle; 5.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; Trypsin; 1.
 DR PIRSF: PIRSF001150; Plasmin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 5.

DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_Ap; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Fibrinolysis; Hydrolyase; Kringle; Plasma; Protease;
 KM Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 FT SIGNAL 1
 FT CHAIN 19
 FT CHAIN 20
 FT CHAIN 20
 FT PEPTIDE 20
 FT CHAIN 97
 FT CHAIN 577
 FT CHAIN 20
 FT DOMAIN 102
 FT DOMAIN 184
 FT DOMAIN 274
 FT DOMAIN 370
 FT DOMAIN 475
 FT DOMAIN 577
 FT ACT_SITE 618
 FT ACT_SITE 661
 FT ACT_SITE 661
 FT ACT_SITE 756
 FT DISULFID 53
 FT DISULFID 103
 FT DISULFID 124
 FT DISULFID 152
 FT DISULFID 185
 FT DISULFID 188
 FT DISULFID 206
 FT DISULFID 234
 FT DISULFID 275
 FT DISULFID 296
 FT DISULFID 324
 FT DISULFID 371
 FT DISULFID 392
 FT DISULFID 420
 FT DISULFID 476
 FT DISULFID 497
 FT DISULFID 526
 FT DISULFID 563
 FT DISULFID 573
 FT DISULFID 603
 FT DISULFID 695
 FT DISULFID 725
 FT DISULFID 752
 SQ SEQUENCE 806 AA; 90981 MW; 95PAA86DC2064D5 CRC64;
 Query Match 75.3%; Score 1160; DB 1; Length 806;
 Best Local Similarity 71.7%; Pred. No. 7; 9e-80;
 Matches 185; Conservative 34; Mismatches 39; Indels 0; Gaps 0;
 QY 1 VVLSBCKTNGKNGVYGTMSKTNGITQCKMSSTSPHPRFPSPATHPBGLSENYCRNPDN 60
 DB 98 IYLSDBCKSGNGVNYGTLSKTSGITQCKMSDLSPHVPRVAPSKYPDAGLEKNGCRNPD 157
 QY 61 DPQGPWCYTTDPKRYDYCDILFCEBCECHGSGENYDGIKSTMGLEQANDSQSPH 120
 DB 158 DVKGPWCYTTNDIRIYCYDVECEBCECHGSGENYRGITISTESGIECQPMDSQSPH 217
 QY 121 GYIPSKFPKNGKNGVCRNPRELAPWCCTTDPNKRMBELCDIPRCTPPSPSGPTQCK 180
 DB 218 EYIPSKFPKDKLENGCRNPDGPRPWCFTSPERKMECNIPRCSSPPPPGPMQCK 277
 QY 181 GTGENTYRGVAVTASGHTQHSAAQTPTHTERTPENPCKNDENYCRNPDGKAPWCHT 240


```

Db      278 GGENYRGKIAVTKSGHTQRMWKCQPHKRNTPENFPCRGIDENYCRNPDELEPWCT 337
QY      241 TMSQVMEYCKIPSCDSS 258
Db      338 TNPVROEYCALPSCGTS 355

RESULT 15
Q6PBA6 BRARE
ID Q6PBA6 BRARE PRELIMINARY; PRT; 818 AA.
AC Q6PBA6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Plasmimogen.
GN Name=pig;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059801; AAH59801.1; -, mRNA.
DR HSSP; P00747; 1B21.
DR ZFIN; ZDB-GENE-030131-1411; plg.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:peptidase activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:00050874; P:organismal physiological process; IEA.
DR GO; GO:00050874; P:organismal physiological process; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan. app.
DR InterPro; IPR01358; Pept_SIA_Plaamin.
DR InterPro; IPR01254; Peptidase_S1_S6.
DR InterPro; IPR01314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.

```

```

DR PIRSF; PIRSF001150; Plasmim. 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 3.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase, Kringle, Protease, Repeat, Serine protease.
SQ SEQUENCE 818 AA; 91636 MW; 55AC014BA38F778 CRC64;

Query Match 64.7%; Score 996; DB 2; Length 818;
Best Local Similarity 61.2%; Pred. No. 2.4e-67;
Matches 158; Conservative 34; Mismatches 66; Indels 0; Gaps 0;

QY 2 YLSECKTGKNGKRYGRTGMSKTKNGITCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 61
DB 106 YLLRFVNGIGMDYRGTKSKTKSGKTCQWEGTFPHVPVITPPRAYPKADLESNFCRNPDD 165
QY 62 PQGPKCYTTDPKRYDQCDILIECEECMHCSENGENYDGKISKTMGLQCAMDSOPHANG 121
DB 166 KGGPWCYTTDPKRYEHCNIDCTECMCQSGENYRGKISTVSGFTQCRWDSQOPONG 225
QY 122 YLSPKPNKNTLKNYCRNPDRRLRPMCFCTTDPNKKMELCDIPRCTTTPPSGPTVQCLKG 181
DB 226 YLPSLPLPKYLEENYCRNPDRGPRPCFTTSSKMKWEACALPRTCTTEPTIYBELTCSAG 285
QY 182 TGENYGNVAVTVSQHTCOHMSAQTPHTERTPENPCKNLIDENYCRNPDGRAPWCHTT 241
DB 286 EGSYRGTSIVTITGKTCQWTSQSPHGRSRSPENYPCKGLDGNVCRNPDRNERSPWCYTT 345
QY 242 NSQVMEYCKIPSCDSSP 259
DB 346 DPEYMEYCSVPSCGDP 363

```

Search completed: January 25, 2006, 17:10:07
 Job time : 163 secs

This Page Blank (uspto)